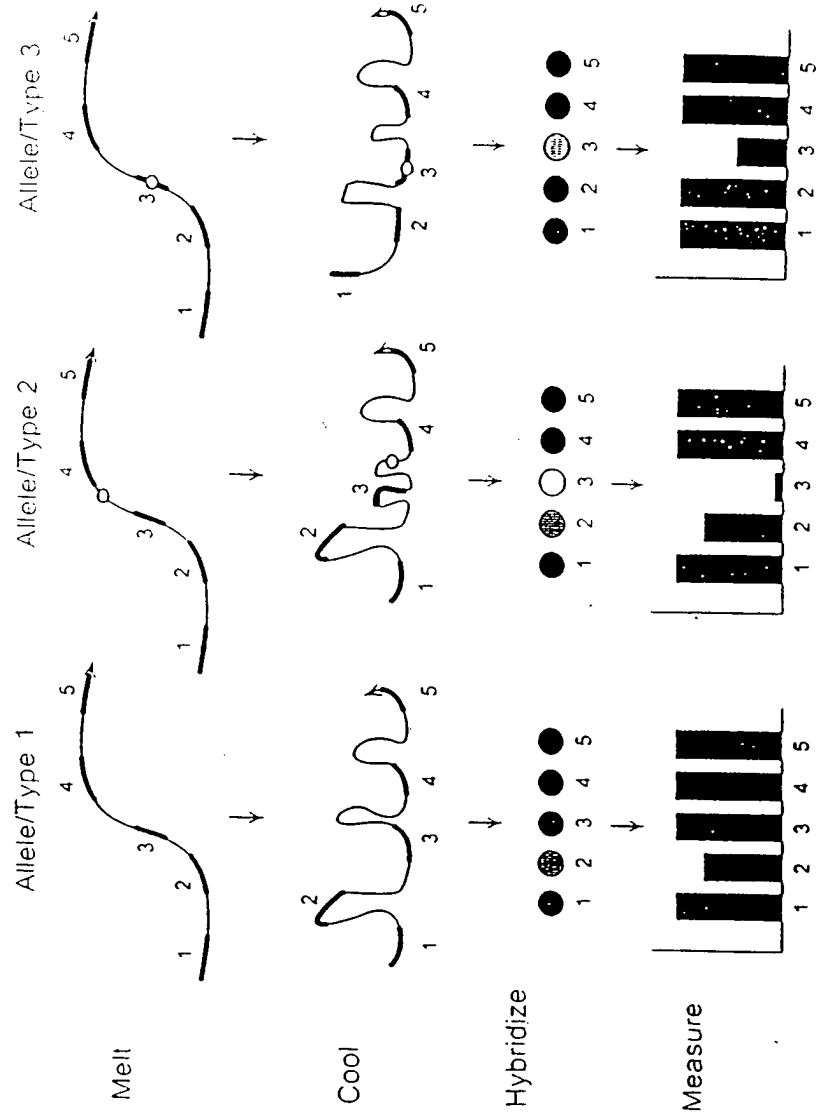


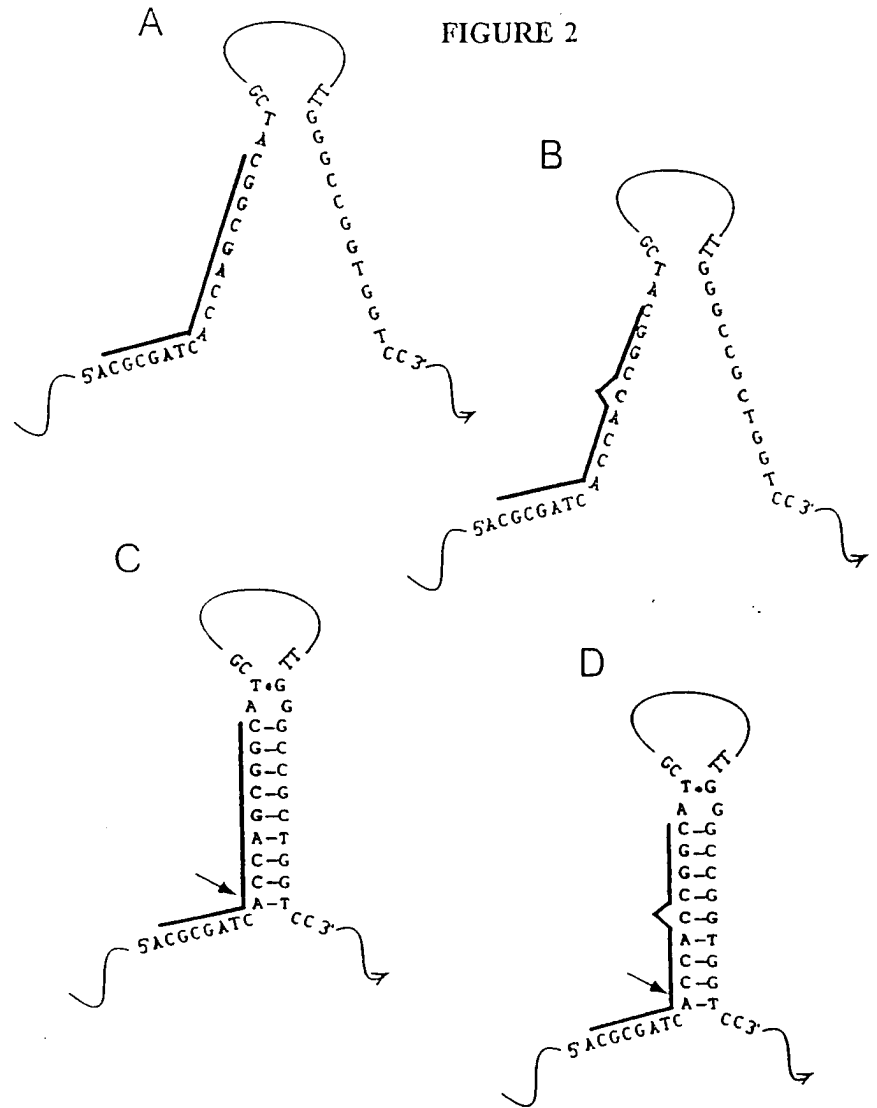
TEST 90" 54628800

FIGURE 1



00882945-061501

FIGURE 2



POSTER-54628860

FIGURE 3

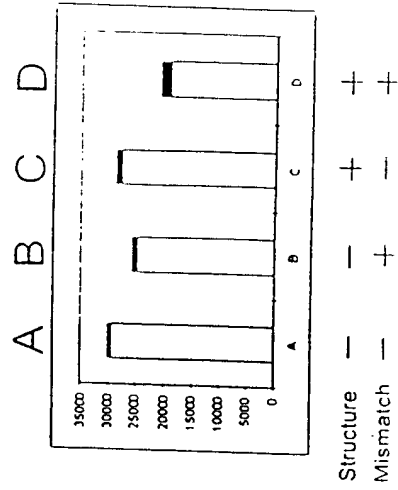
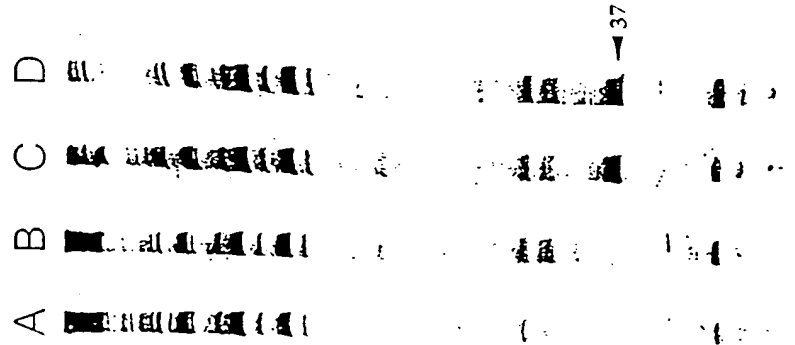
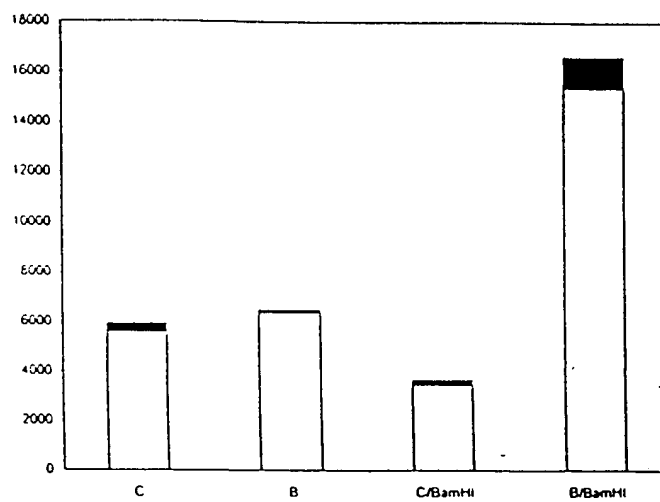


FIGURE 4



00882945-061501

FIGURE 5

09882945-061501

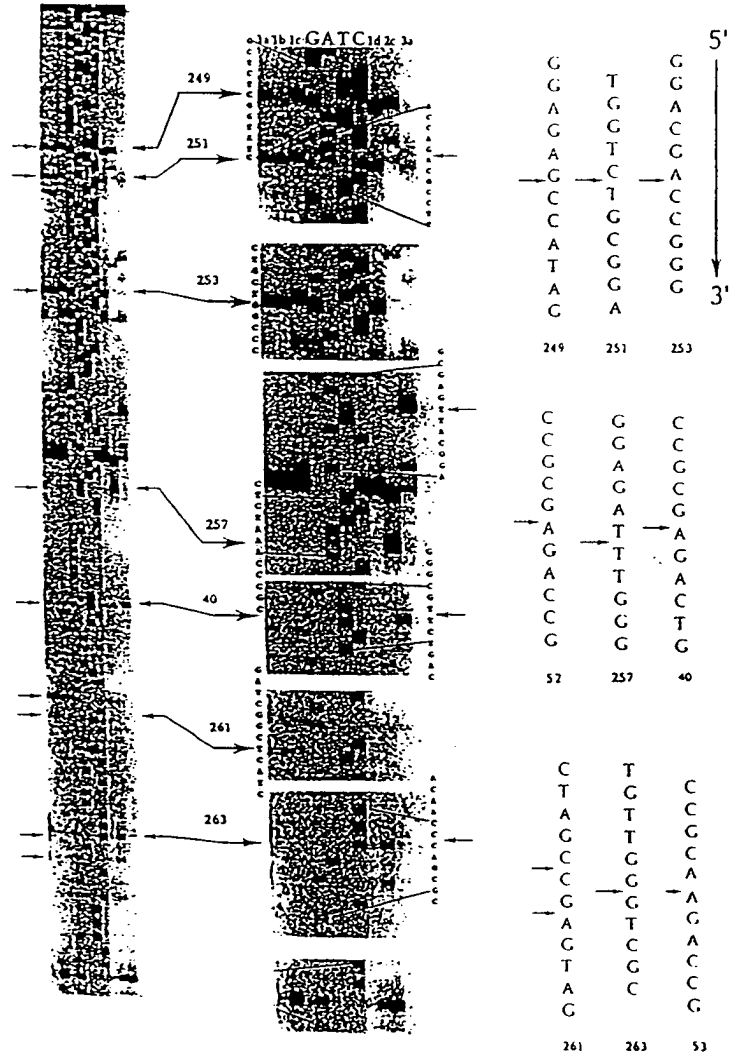


FIGURE 6

Consensus :	GATTCTGTCT	TCACGCAGAA	AGCGTCTAGC	CATGGCGTTA	GTATGAGTGT	CGTGCAGCCT
HCV 1a	-	-	-	-	-	-
HCV 1b	-	-	-	-	-	-
HCV 2c	-	-	-	-	-	-
HCV 3a	-	-	-C-	-	-C-	-A-

[illegible]

#253		#257
<u>TTGCCAGGAC GACCGGTCC</u>	<u>TTTCTGGAT CAACCGCTC</u>	<u>AATGCCTGGA GATTGGGCG</u>
- - - - -	- - - - -	- - - - -
- - - - -	- - - - -	- - - - -
- G- A T- - - -	- - - - -	- - - - -
- C-TG-GT - - - -	- A- - A- -	- T- - C-C C-
- - - - -	- - - - -	- A-CA-A-

[illegible][illegible]

FOGTSU-54628860

FIGURE 7

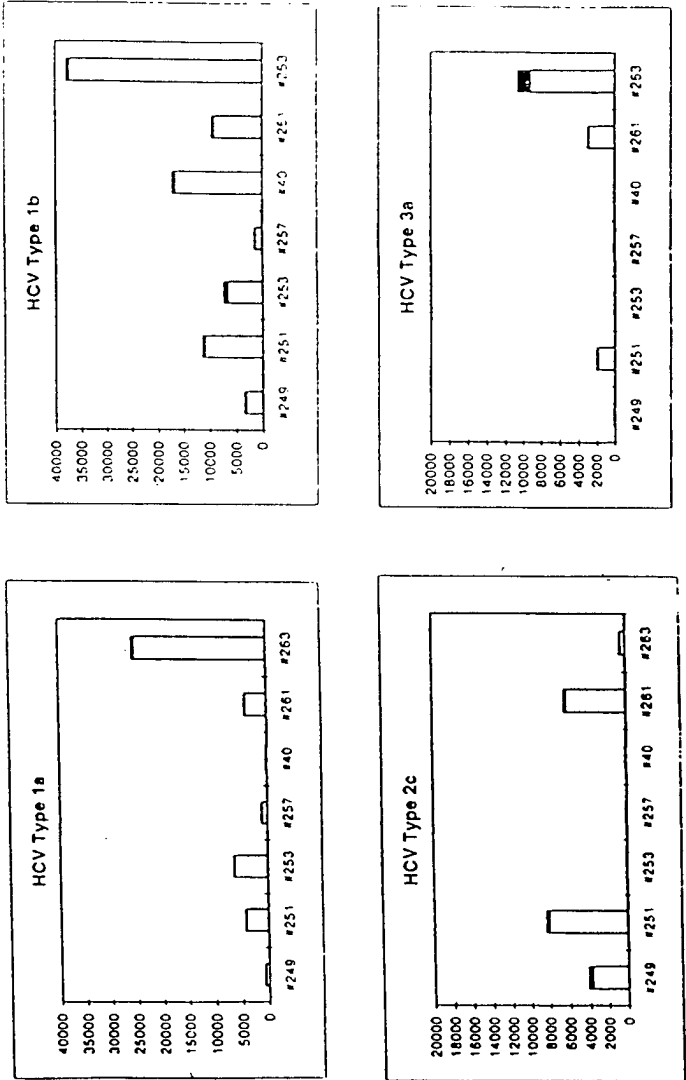


FIGURE 8A

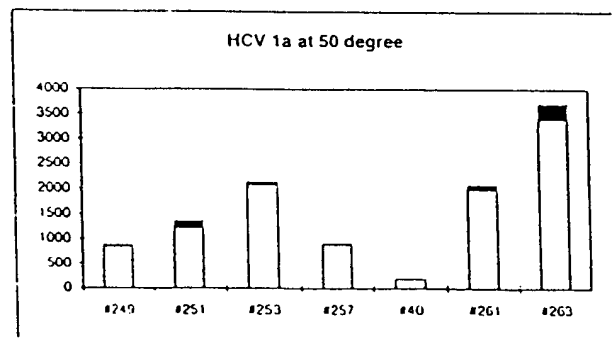
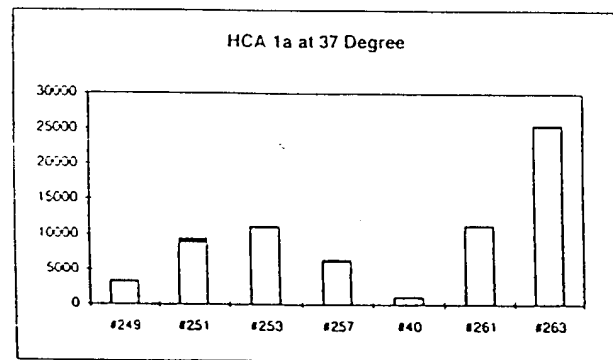
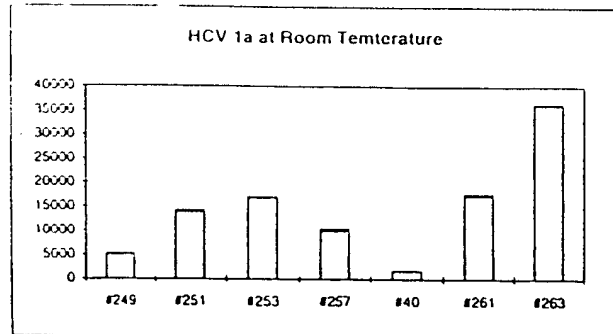
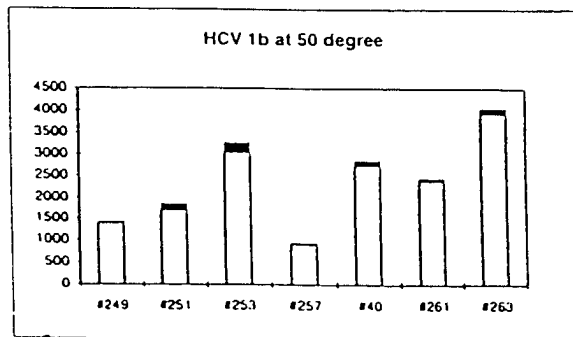
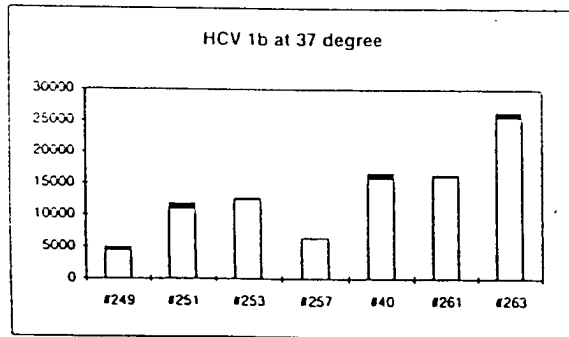
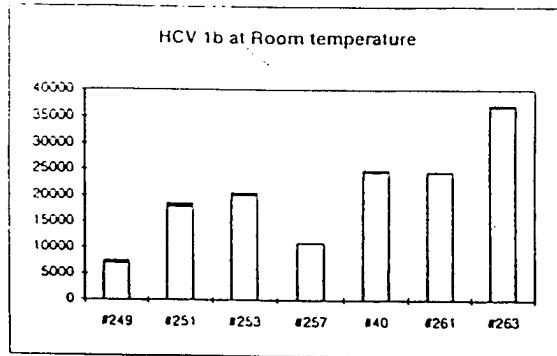
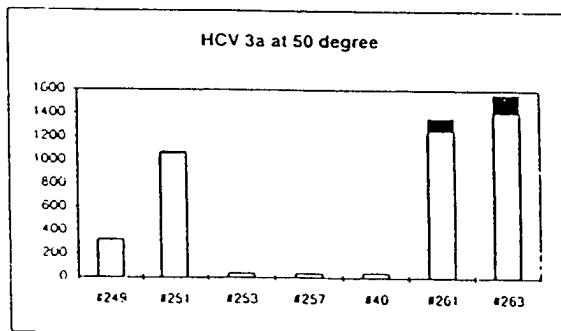
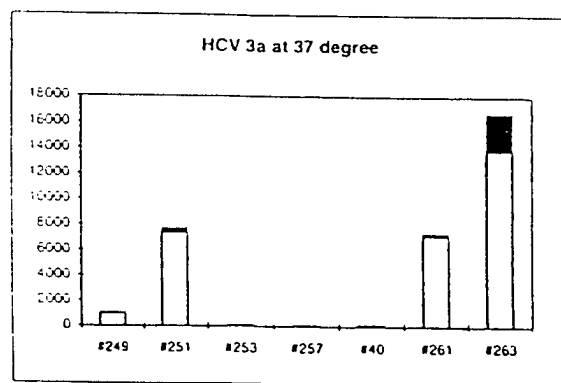
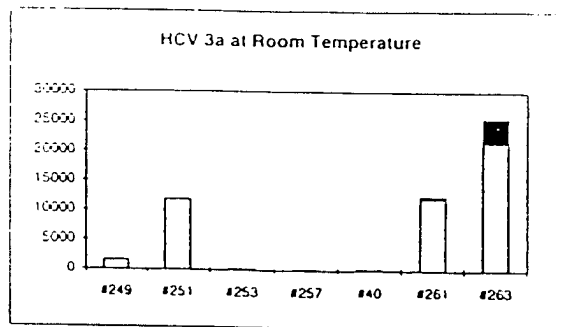


FIGURE 8B



09882945-761504
105190-54628860

FIGURE 8C

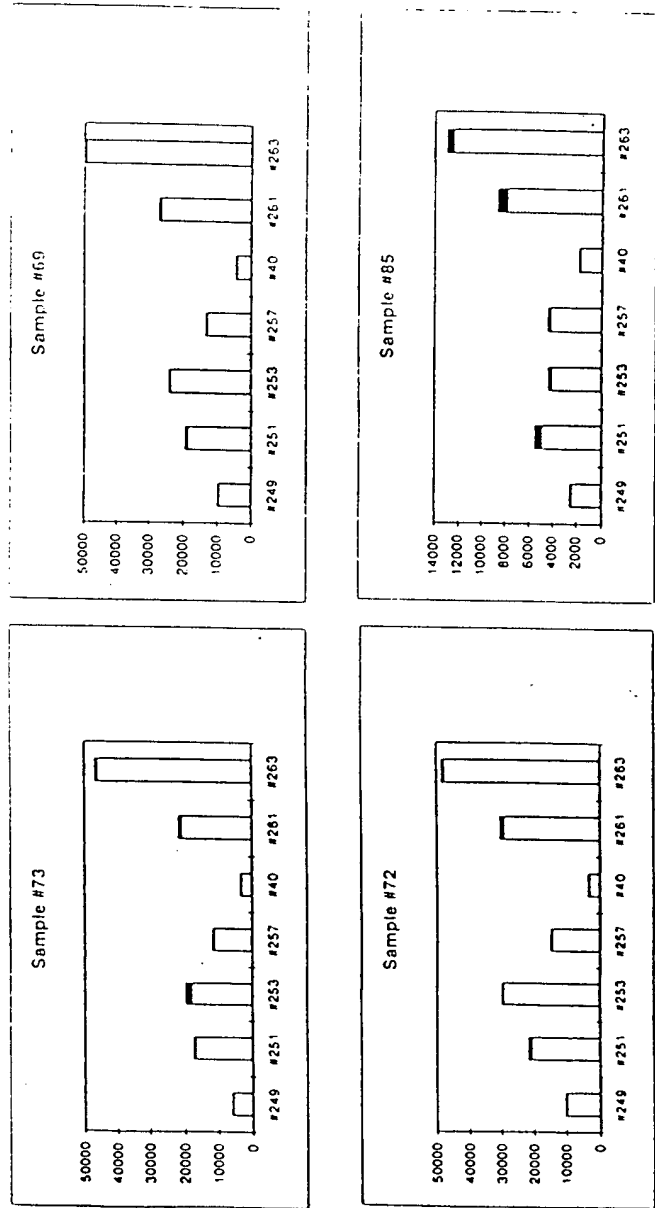


00882943-061501

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TEST 91" 54628800

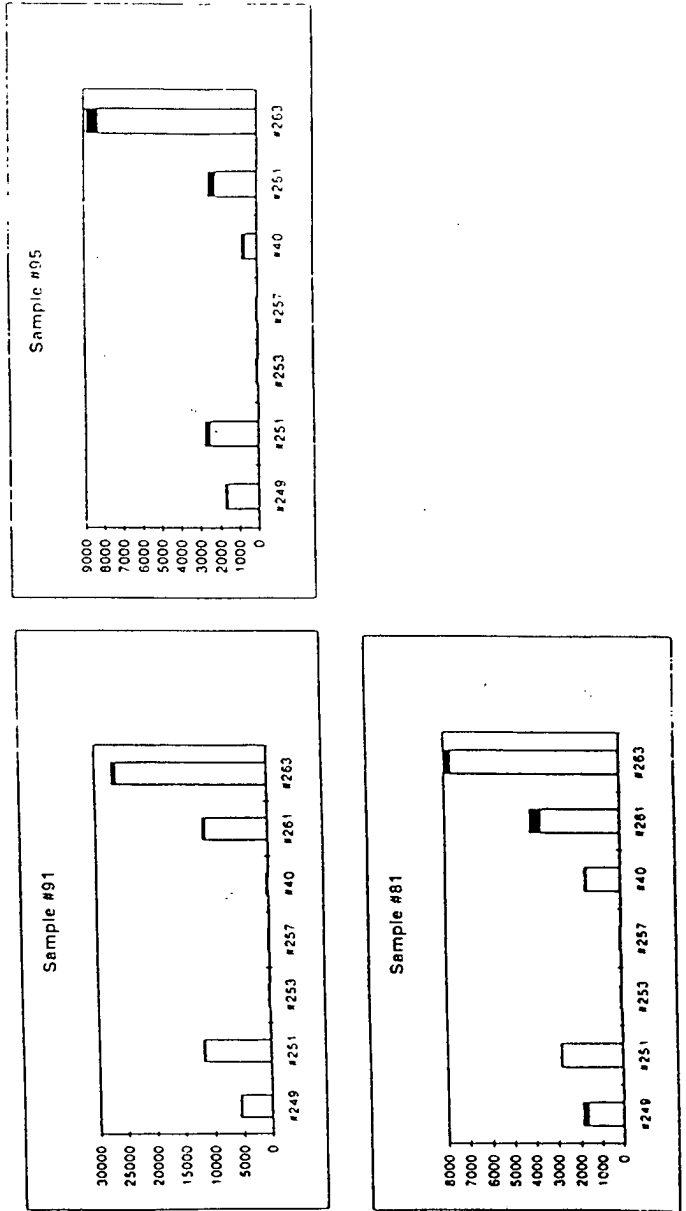
FIGURE 9A



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POSTED 5-16-2000

FIGURE 9B



105150-5162880

FIGURE 9C

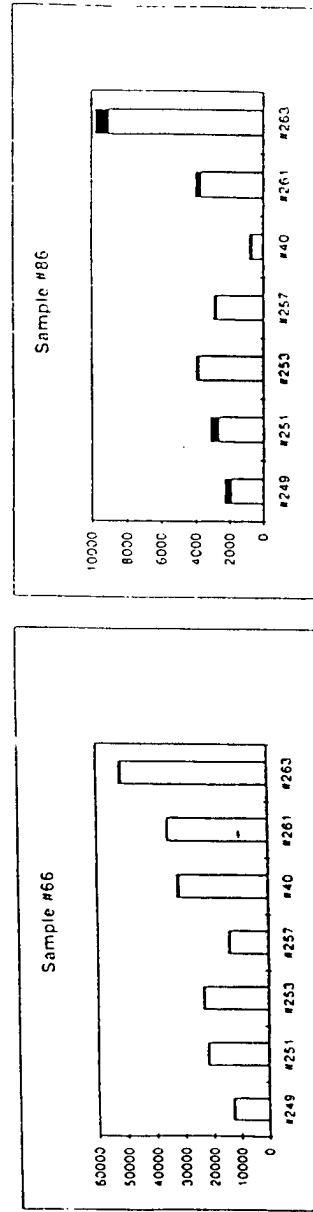


FIGURE 9D

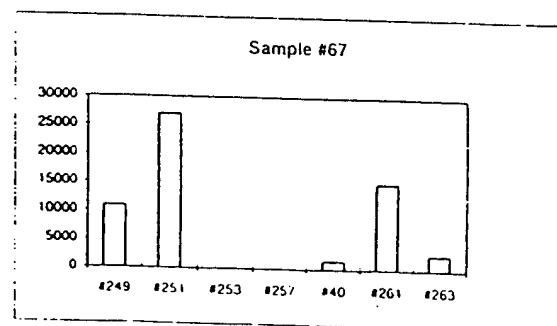
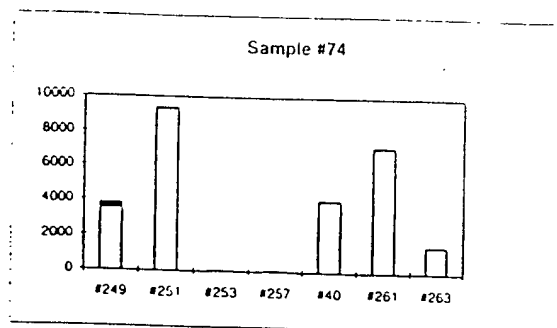


FIGURE 10

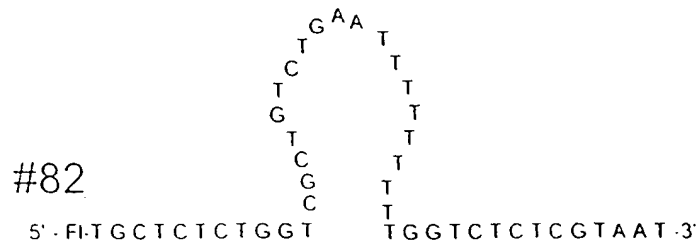
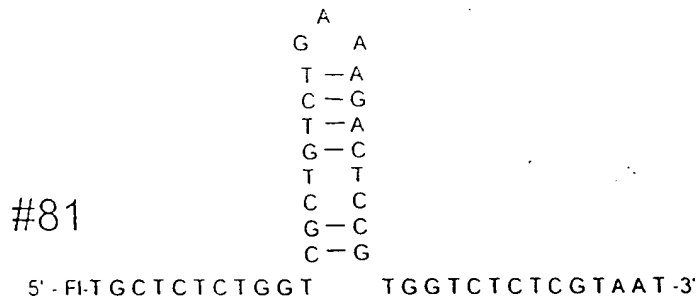
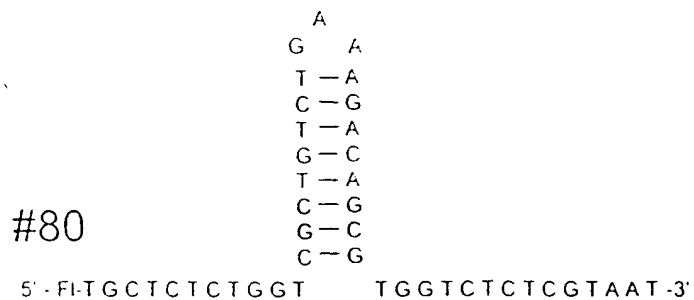


FIGURE 11A

#2) 5' Biotin

```

      I
      T  A
C  G  A
A  T  A
G  C  G
A  T  A
C  G  C
A  T  A
G  C  G
C  G  C
G  C  G

```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#FD91) 3' Biotin - CGAGAGACCA-5'

```

      A
      G  A
      T  A
      C  G
      T  A
      G  C
      T  A
      C  G
      G  C
      C  G

```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - AGACCATTACCAGA -Biotin 5'

#4) 3' - GAGACCATTACCAGAG -Biotin 5'

#79) 3' - AGAGACCATTACCAGAGA -Biotin 5'

↓ ↓

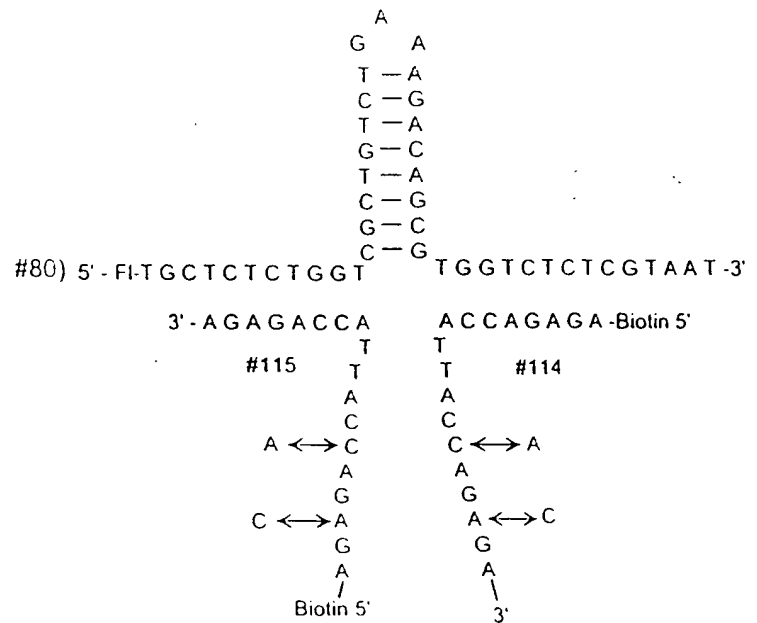
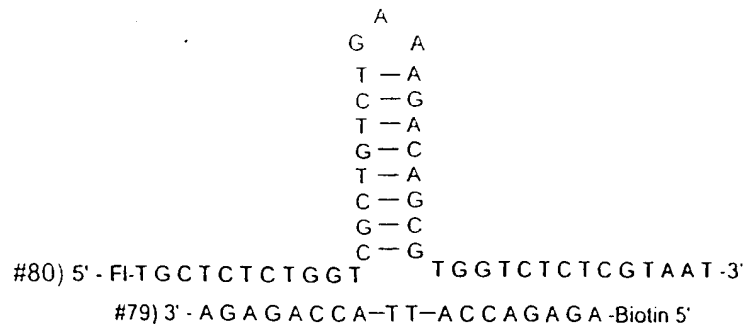
#116) 3' - AGAGACCAACCAGAGA -Biotin 5'

#117) 3' - TACCAGAGA -Biotin 5'

#118) 3' - AGAGACCAT -5'

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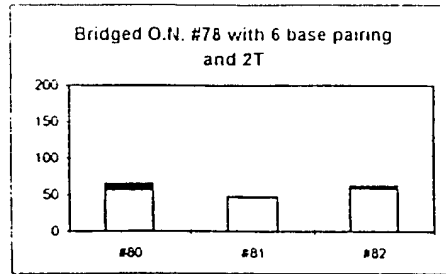
FIGURE 11B



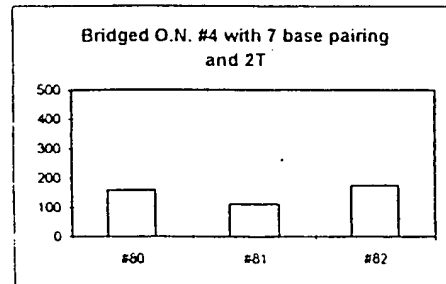
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FIGURE 12

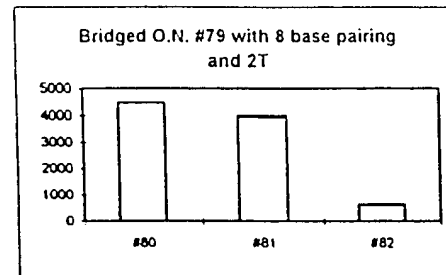
A



B



C



D

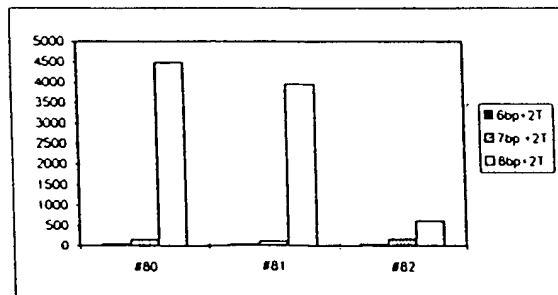
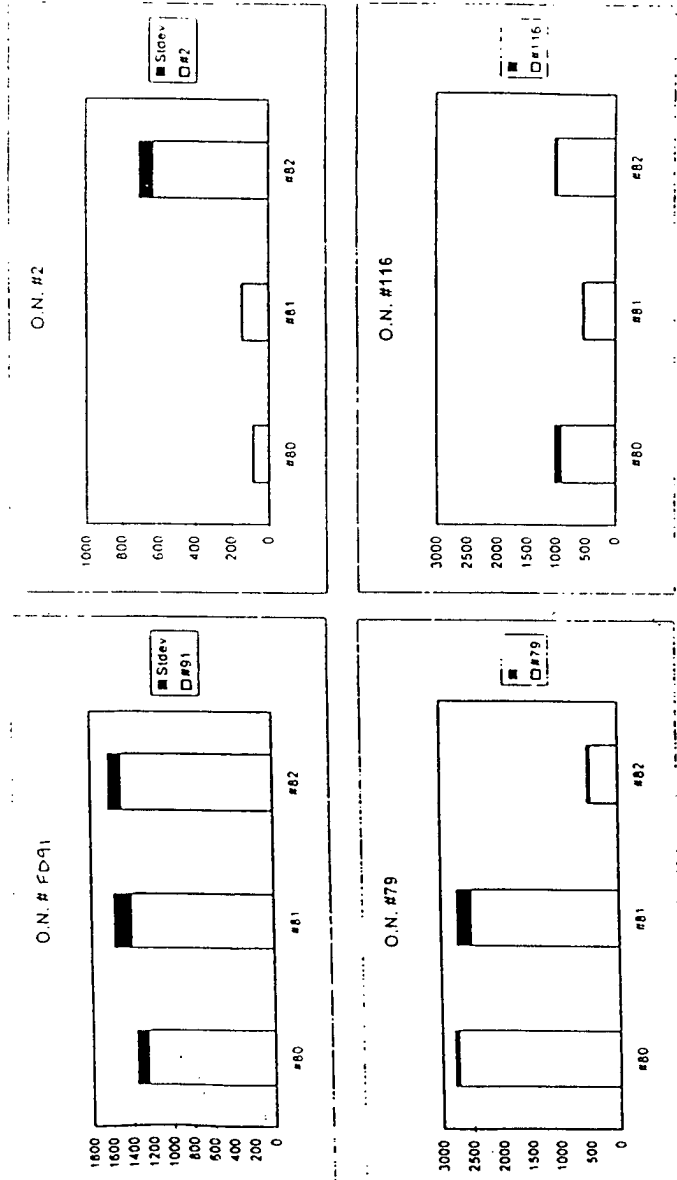


FIGURE 13A

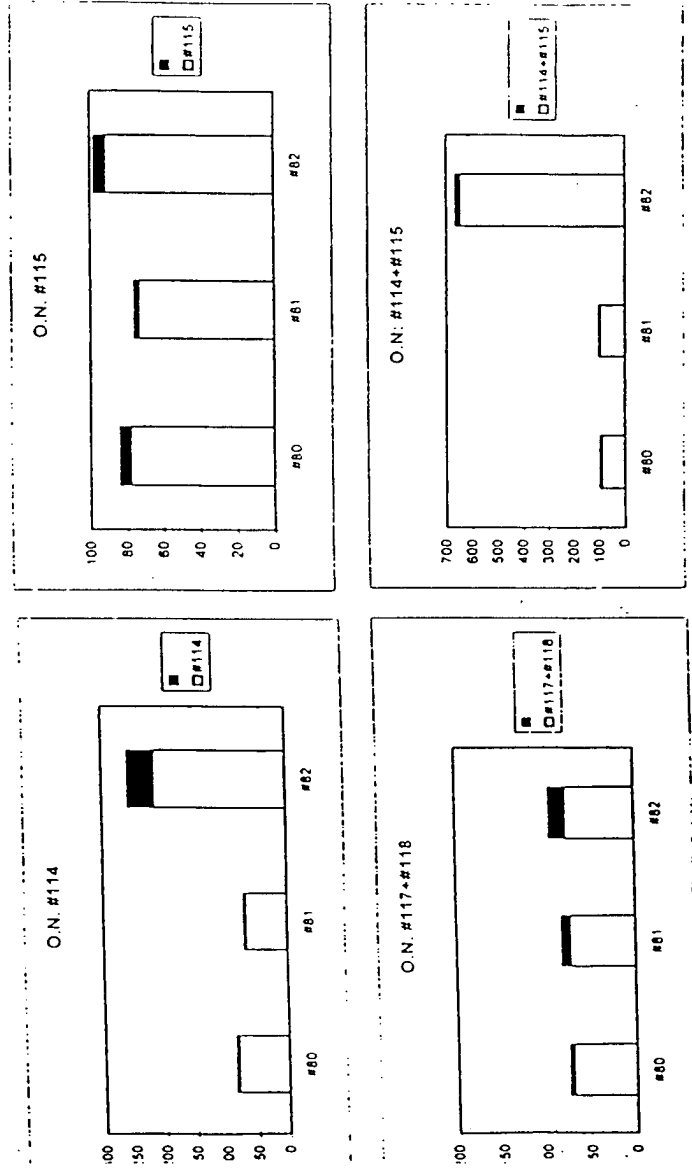
FOIA b7 - D



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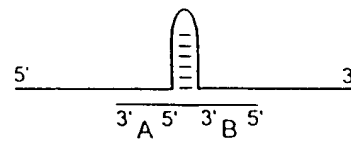
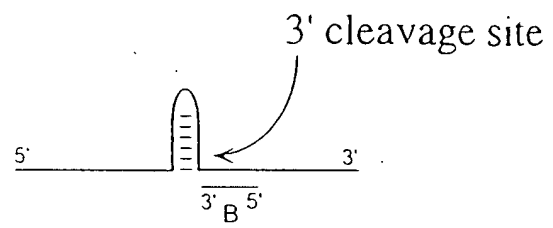
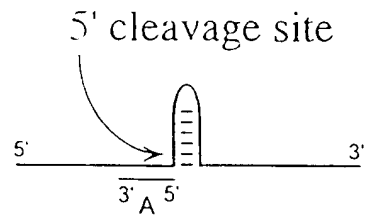
FIGURE 13B

US 5,162,200



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FIGURE 14



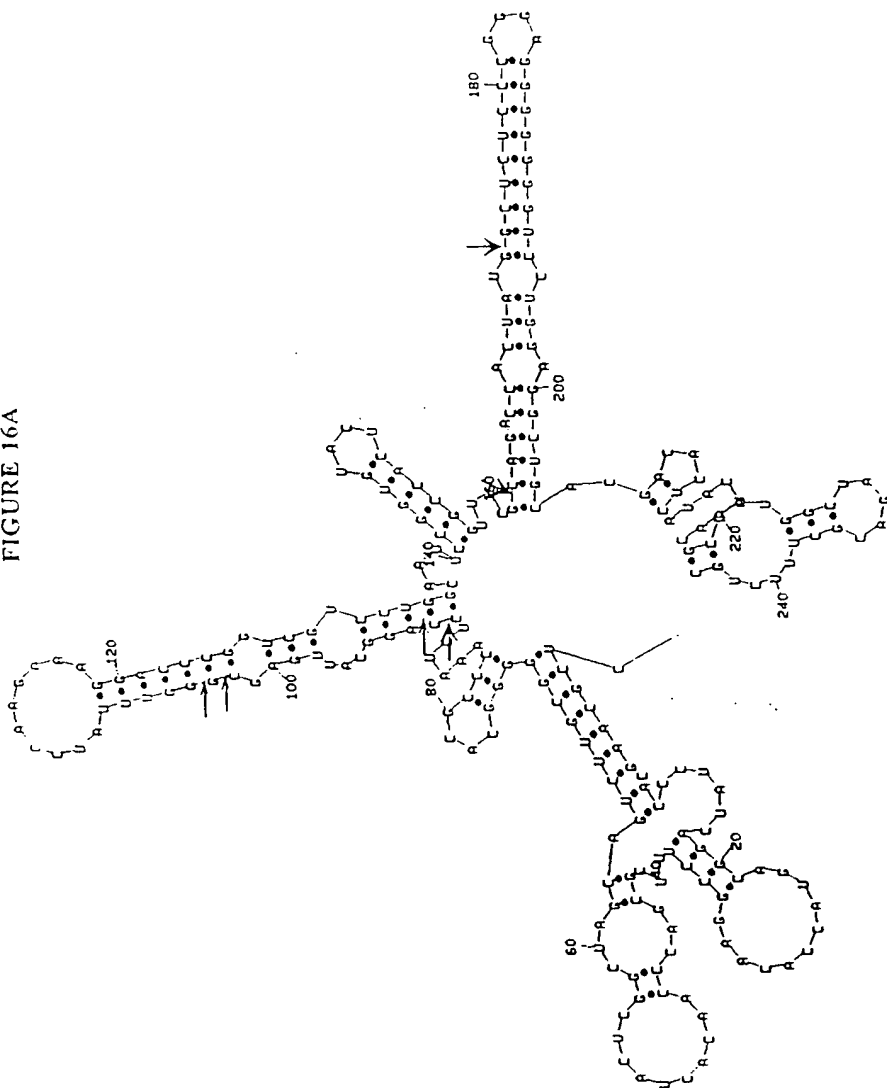
0982945-051501
FOI50-562860

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	1	-----10-----20-----30-----40-----50-----60-----70-----80-----	
1a	CTCGCAAGCACCCATCAGGCACGTACCACAAGGCCCTTTCGGACCCAAACACTACTCGGCTAGCATCTTGCGGGSGCACCG		
1b I I I I C		
2a/c A G		
3a TGA C		
	-----90-----100-----110-----120-----130-----140-----150-----160-----		
1a	CCCCAATCTC TAGGCATTGACCGGTTTATCCAGAAGGACCCGGTCGTCCTGGCAATTCCGGTGTACTACACCGGTTCC		
1b I I G I I		
2a/c GG G A T C		
3a T TG T CT AC CA CG		
	-----170-----180-----190-----200-----210-----220-----230-----240-----		
1a	CCAGACCACTATGGCTCTCCGGAGGGGGGGTCTGGAGGCTGCACGACACTCATACTAACCCCATCGCTAGACGGCTTTCGCG		
1b	I I I I I		
2a/c I I G T		
3a	I I I I G		

105190 CH62886U

FIGURE 16A



FOSTED-5162864

FIGURE 16B

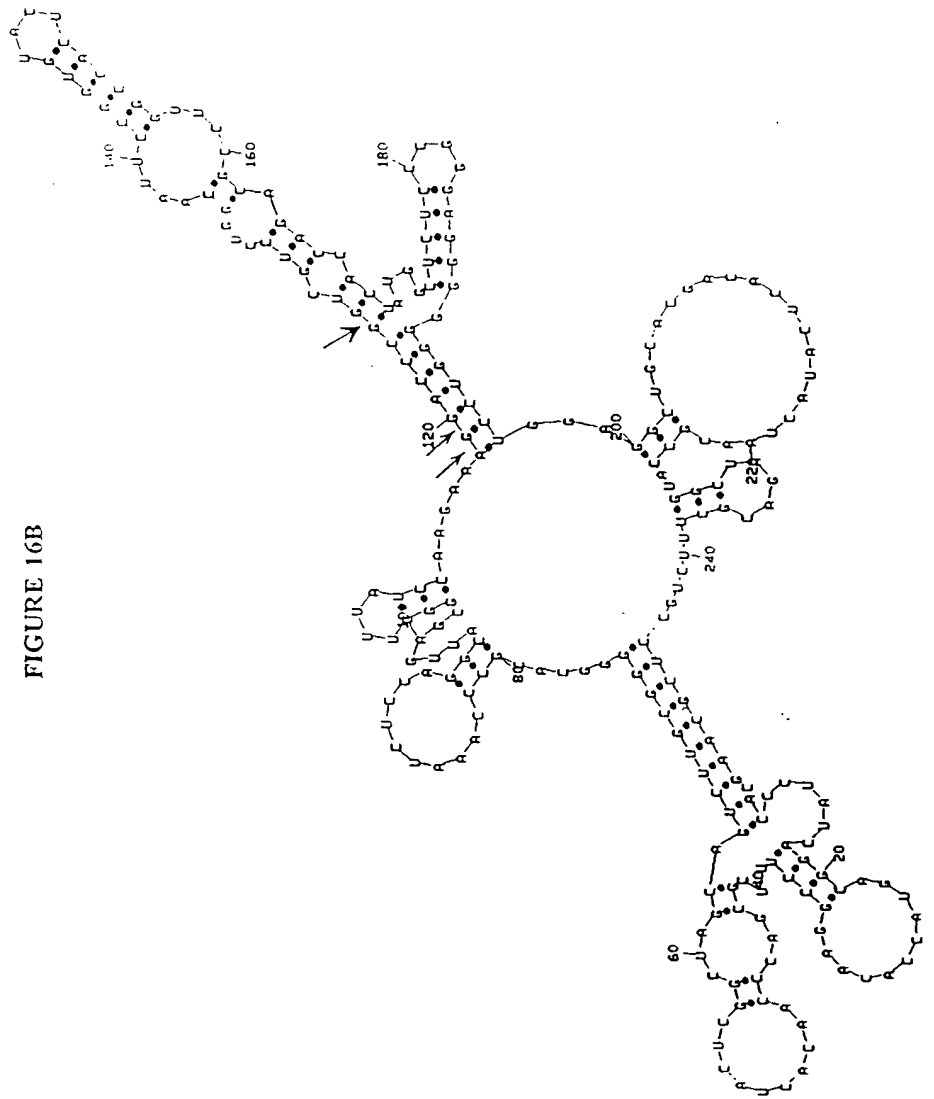
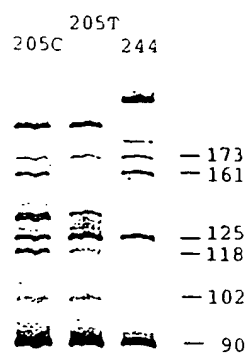


FIGURE 17A



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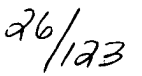
[illegible]

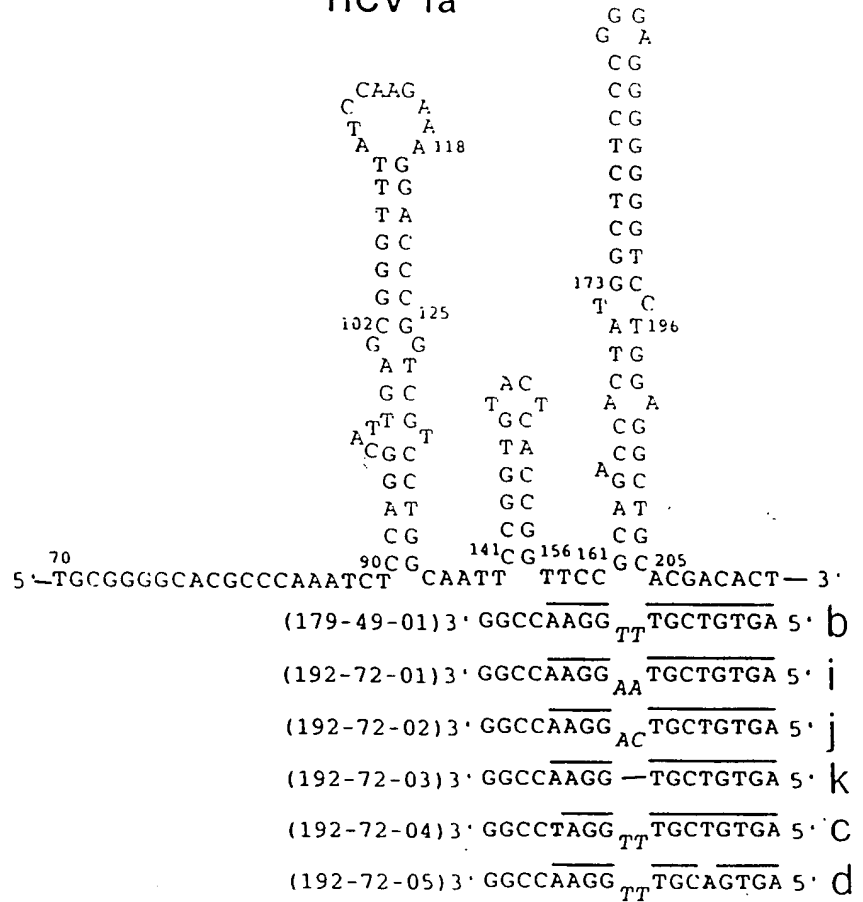
FIGURE 17C

5' Biotin ——— TCCAAGAA GGAGGCTG ——— 3'

m (#81-04) 3'-AGGTTCTTCCCTCCGAC-5'

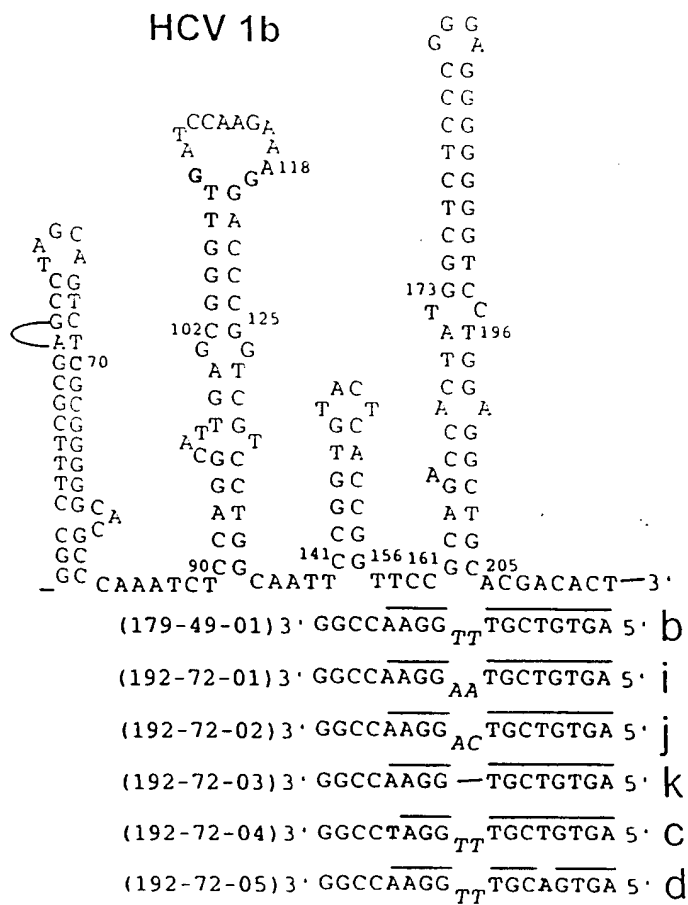
FIGURE 18A

HCV 1a



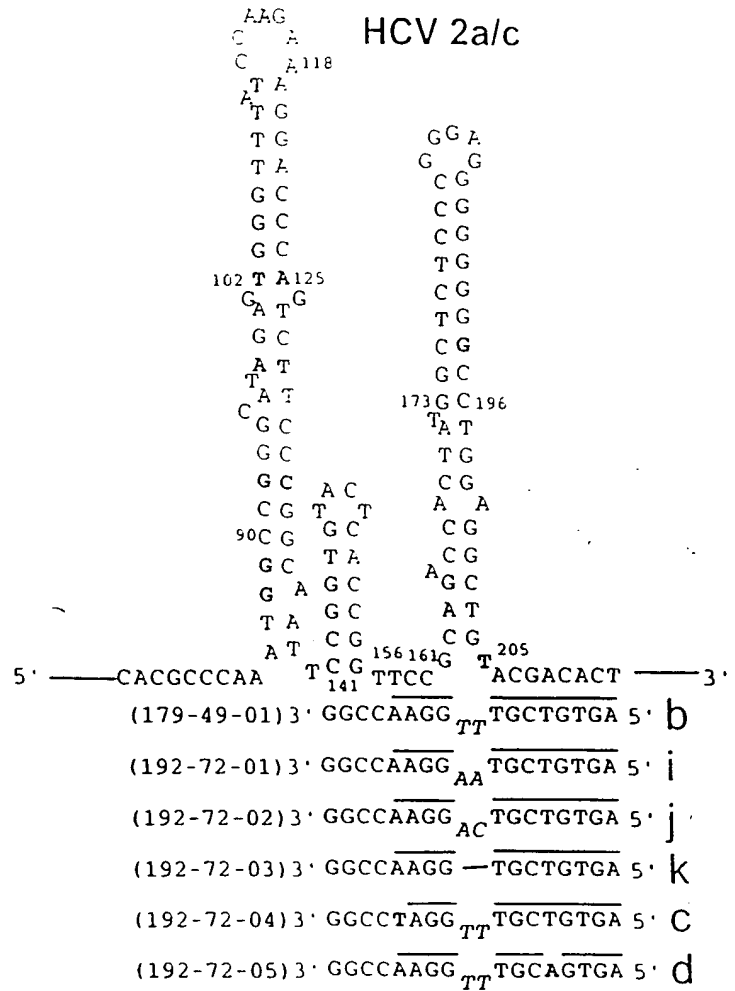
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FIGURE 18B



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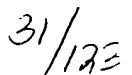
FIGURE 18C



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HCV 3a



TESTED 5462860

FIGURE 19

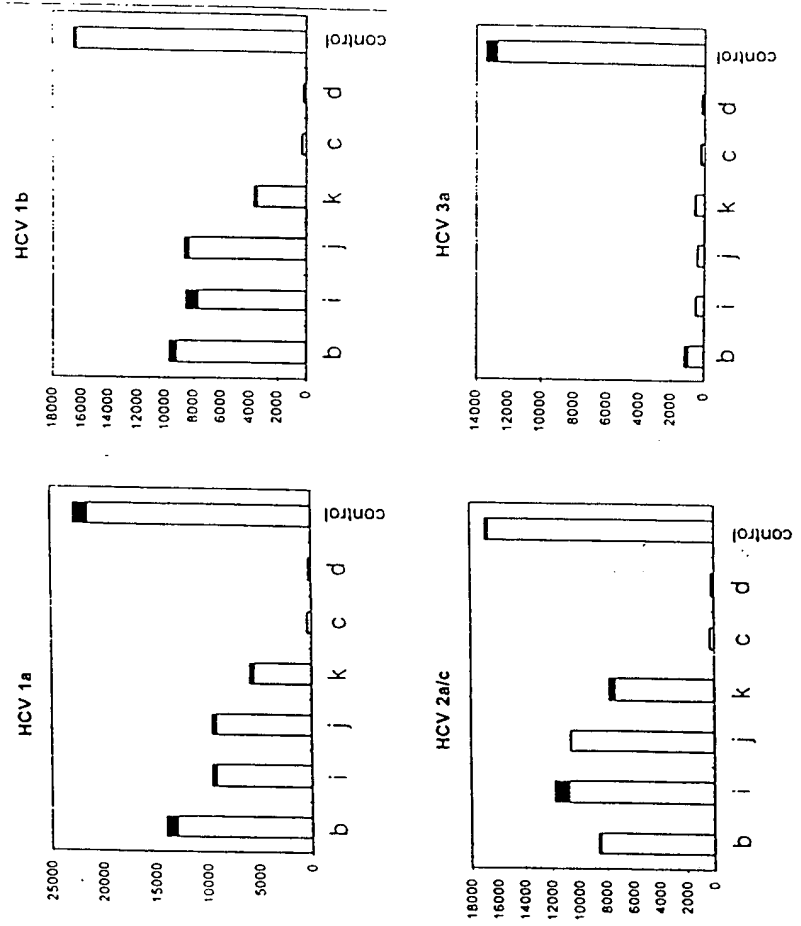


FIGURE 20A

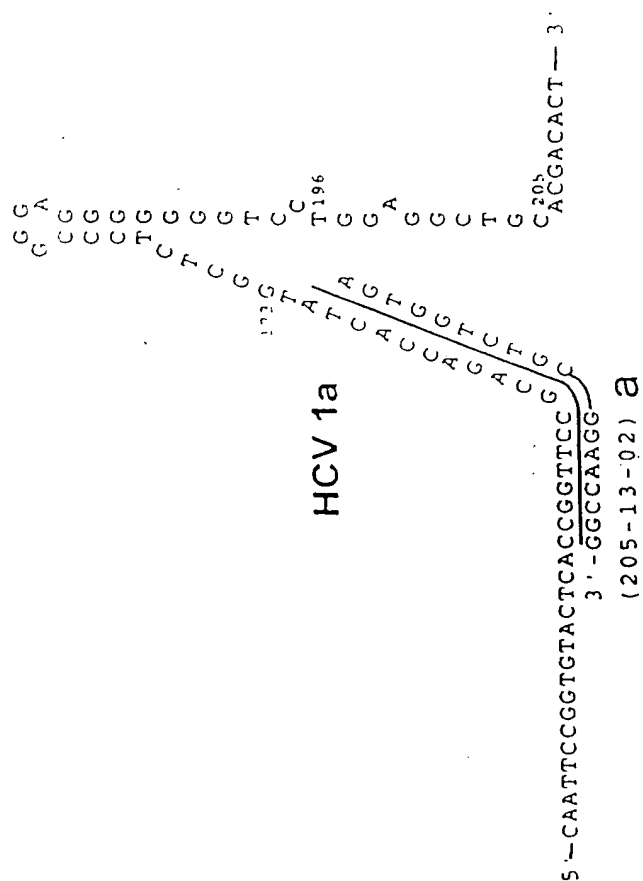
FIGURE 20A

G G
 G A
 C G
 C G
 C G
 T G
 C G
 T G
 C G
 G T
 173 G C
 T C
 A T¹⁹⁶
 T G
 C G
 A A
 C G
 C G
 A G C
 A T
 C G
 5'-CAATTCCGGTGTA CACCGGTTC G C²⁰⁵ ACGACACT-3'

HCV 1a

- a 3'-GGCCCAAGGCGTCTGGTGA-F1.5' (205-13-02)
- b 3'-GGCCCAAGG_{TT} TGCTGTGA F1.5' (179-49-01)
- c 3'-GGCCCTAGG_{TT} TGCTGTGA F1.5' (192-72-04)
- d 3'-GGCCCAAGG_{TT} TGCAGTGA F1.5' (192-72-05)
- e 3'-GGCCCAAGG-F1.5' (205-27-01)

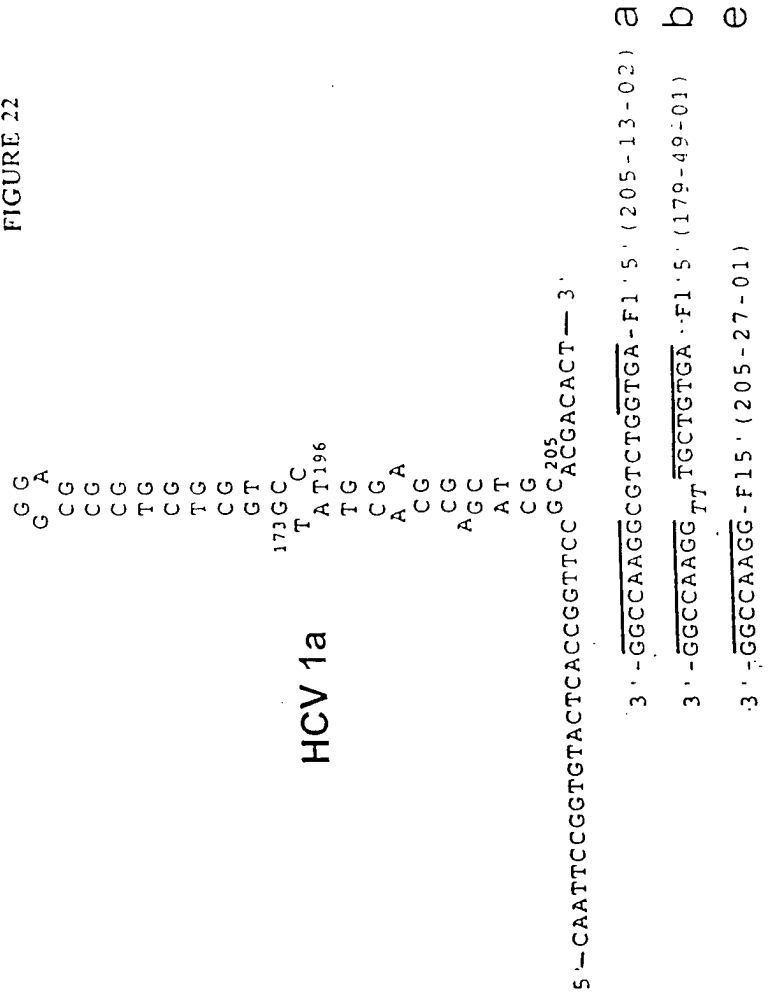
FIGURE 20B



[illegible]

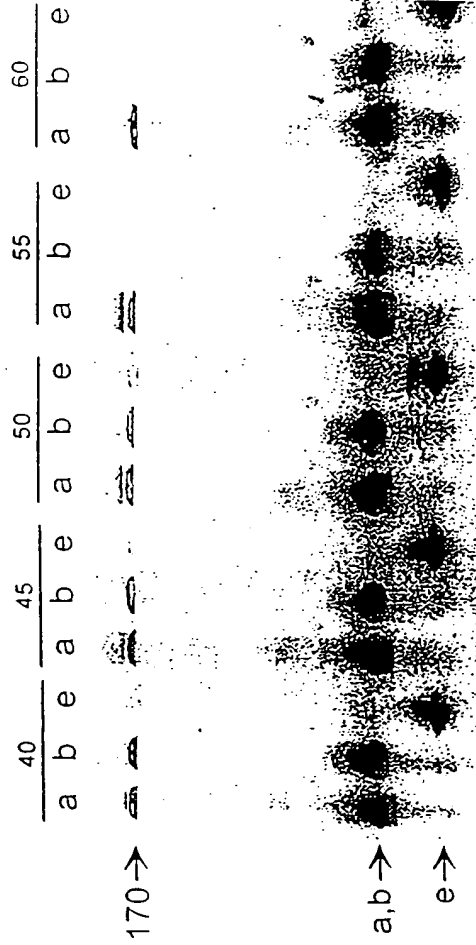
105190* 57622860

FIGURE 22



105190-51628860

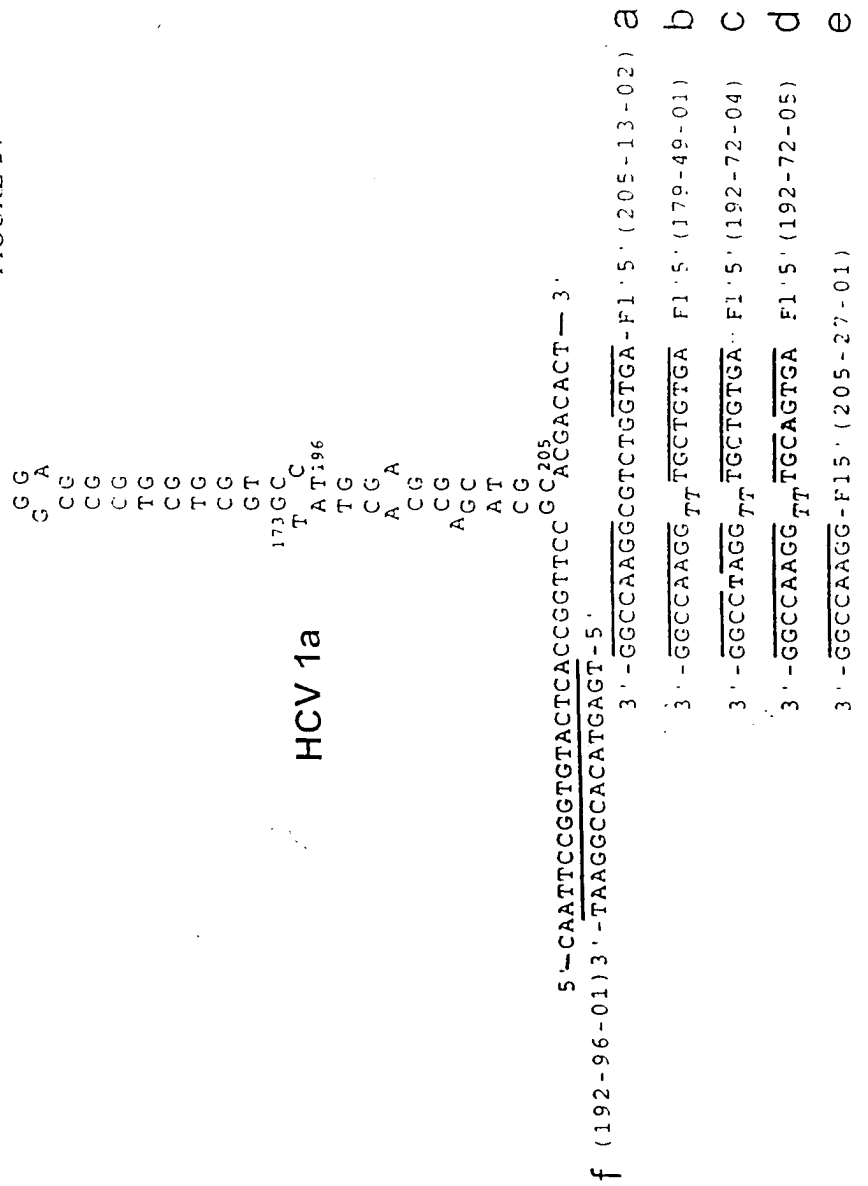
FIGURE 23



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POST 90-54628860

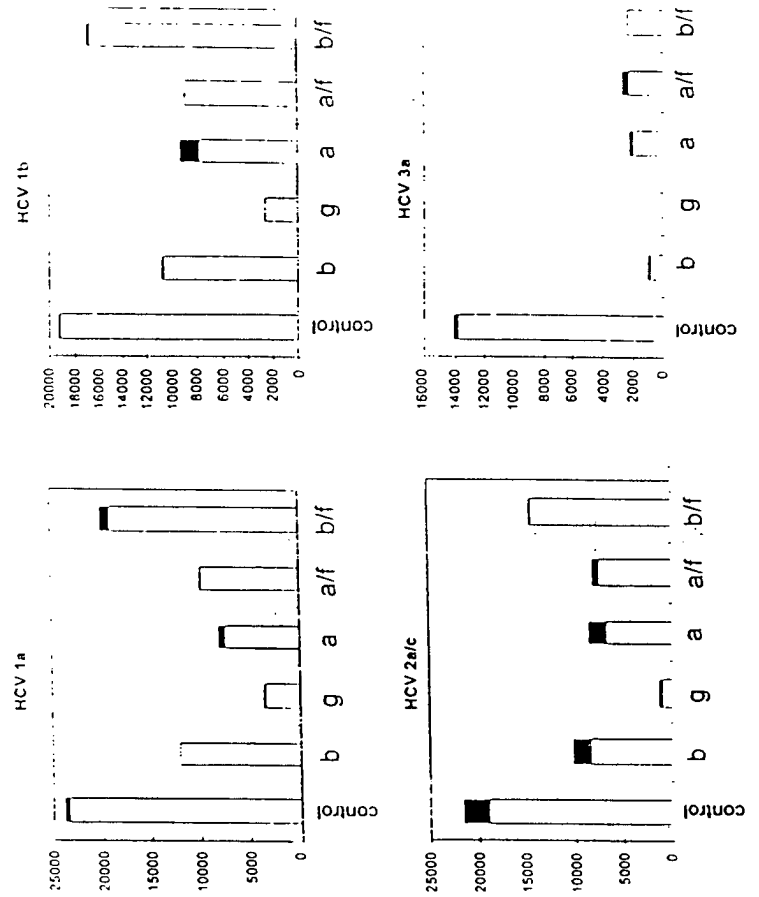
FIGURE 24



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FIGURE 25



POST 90-54628860

FIGURE 26

5'-ATTCCGGTGTACTACCGGTTCCAAACGACACT-3' (205-13-01) S.T.
f (192-96-01) 3'-TAAGGCCACATGAGT-5'
3'-GGCCAAAGCGCTCTGGTGA-F1'5' (205-13-02) a
3'-GGCCAAAGG_{TT}TGCTGTGA-F1'5' (179-49-01) b
3'-GGCCTAGG_{TT}TGCTGTGA-F1'5' (192-72-04) c
3'-GGCCAAAGG_{TT}TGCAGTGA F1'5' (192-72-05) d
3'-GGCCAAAGG-F15' (205-27-01) e

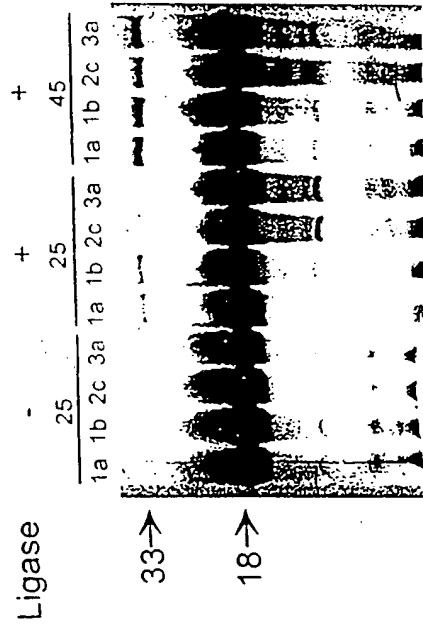
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FIGURE 27


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105190-54628860

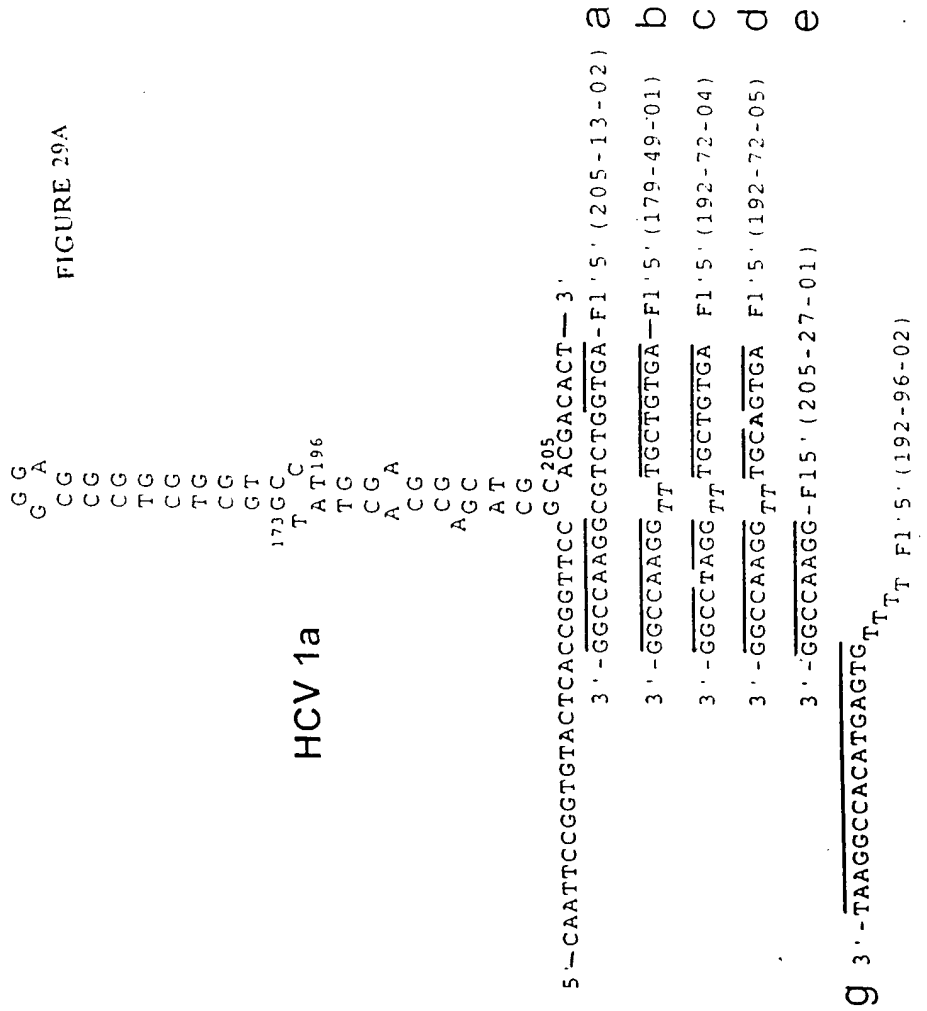
FIGURE 28



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105191154628660

FIGURE 29A



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TDSF90-51628860

FIGURE 29B

5' - ATTCCGGTGTA CTACCGGTCCAAAGCACACT - 3' (205-13-01) S.T.
3' - GGCCAAAGCGTCTGGTGA - F1'5' (205-13-02) a
3' - GGCCAAAGG TT TGCTGTGA - F1'5' (179-49-01) b
3' - GGCCTAGG TT TGCTGTGA - F1'5' (192-72-04) c
3' - GGCCAAAGG TT TGCAGTGA - F1'5' (192-72-05) d
3' - GGCCAAAGG - F15' (205-27-01) e
g 3' - TAAGGCCACATGAGTG TT TT - F1'5' (192-96-02)

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FIGURE 31

G G
G A

CG

CG

CG

TG

CG

TG

CG

GT

177 GC

T AT196

TG

CG

A A

CG

AGC

AT

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

CG

HCV 1a

5'-CAATTCCGGTGCTACTCACCAGTTCC C²⁰⁵ ACGACACT - 3'

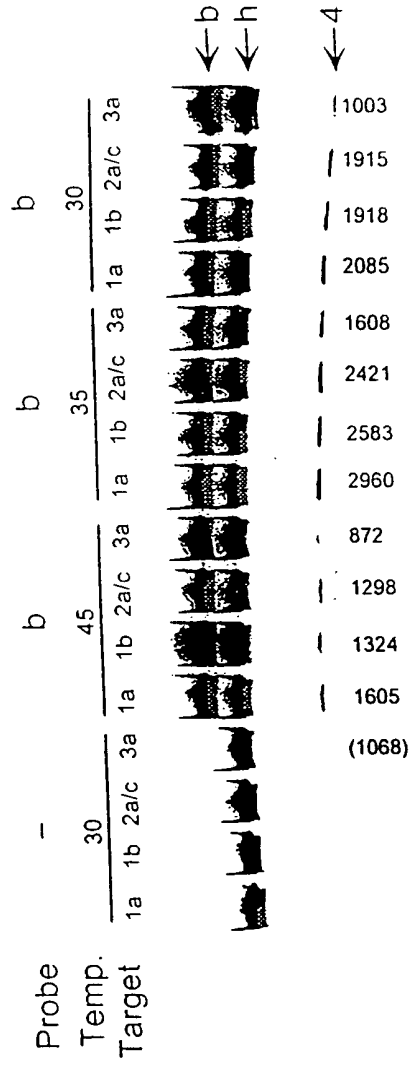
3'-GGCCAAGG TT TGCTGTGA -Fl 5' (179-49-01)

b

h (10 bp) 3'-CACATGAGTG T_T T_T -Fl 5' (205-81-01)

FO5F90-51628860

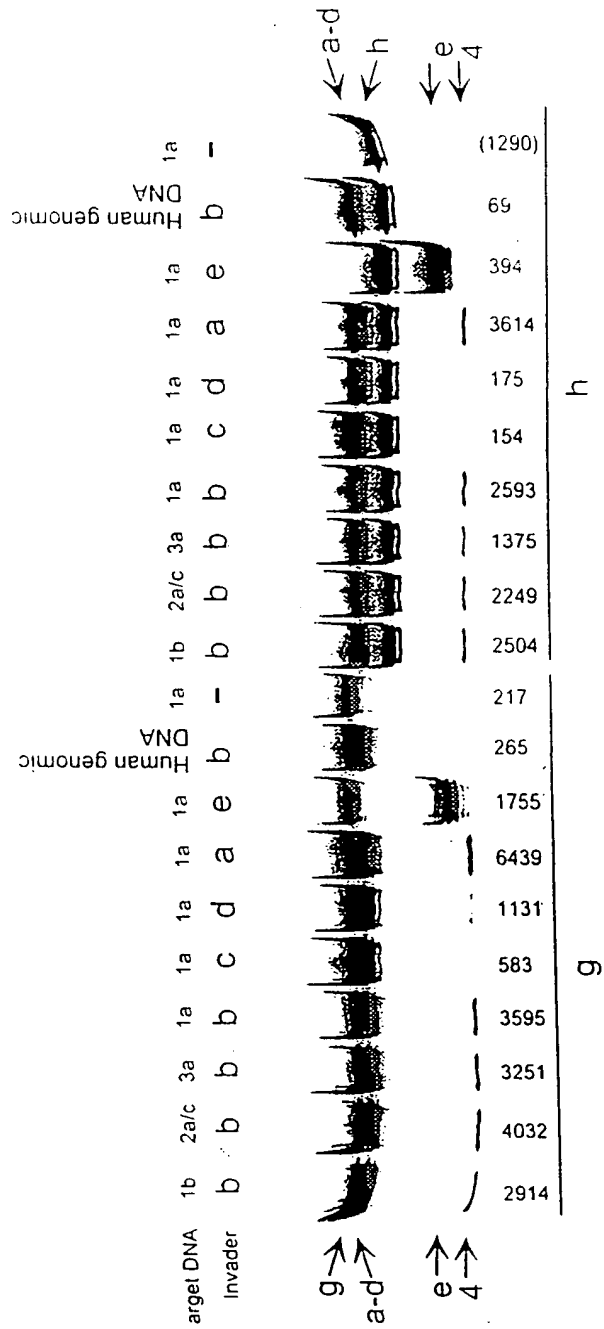
FIGURE 32



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105T01 51628800

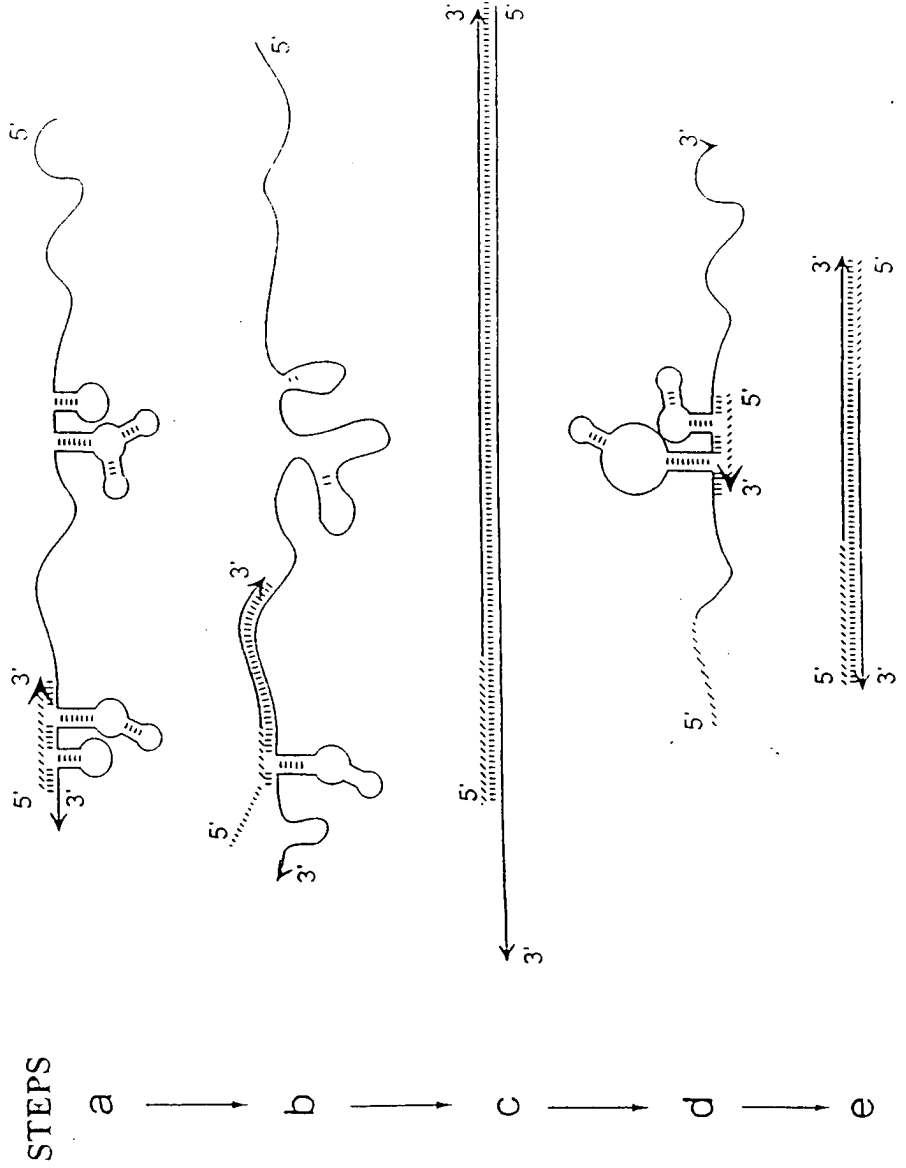
FIGURE 33



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POST 93-5102860

FIGURE 34



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STEPS

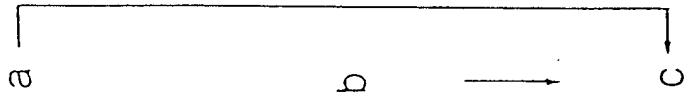
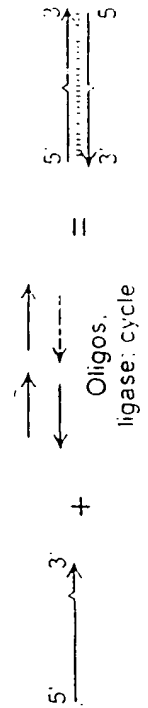
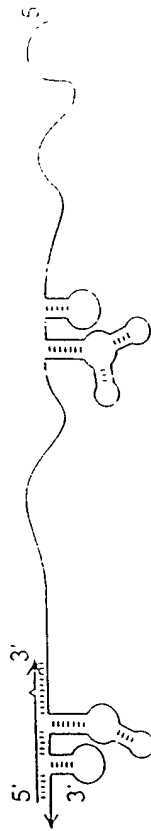
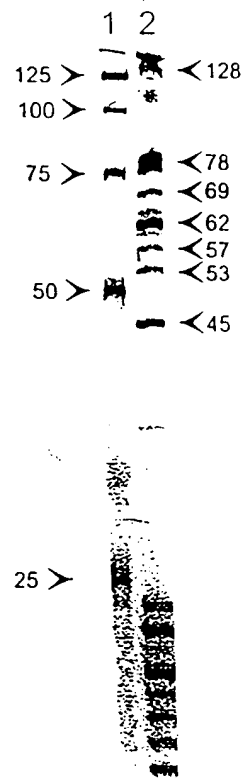


FIGURE 35



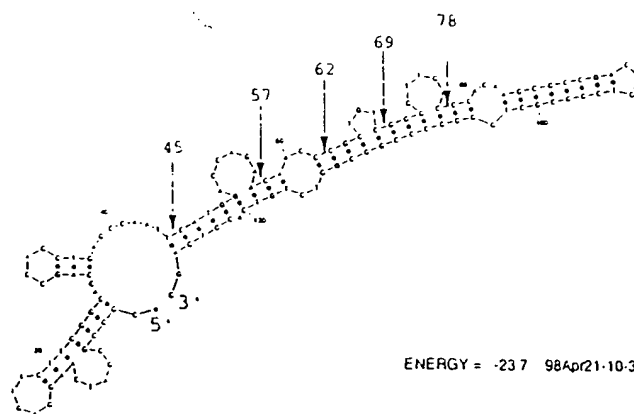
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FIGURE 36

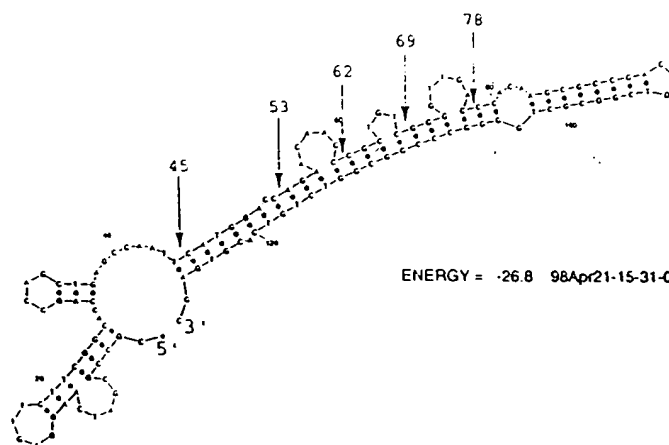


00882945-061501

FIGURE 37A



ENERGY = -23.7 98Apr21-10:39:54



ENERGY = -26.8 98Apr21-15:31:05

008629415-061501

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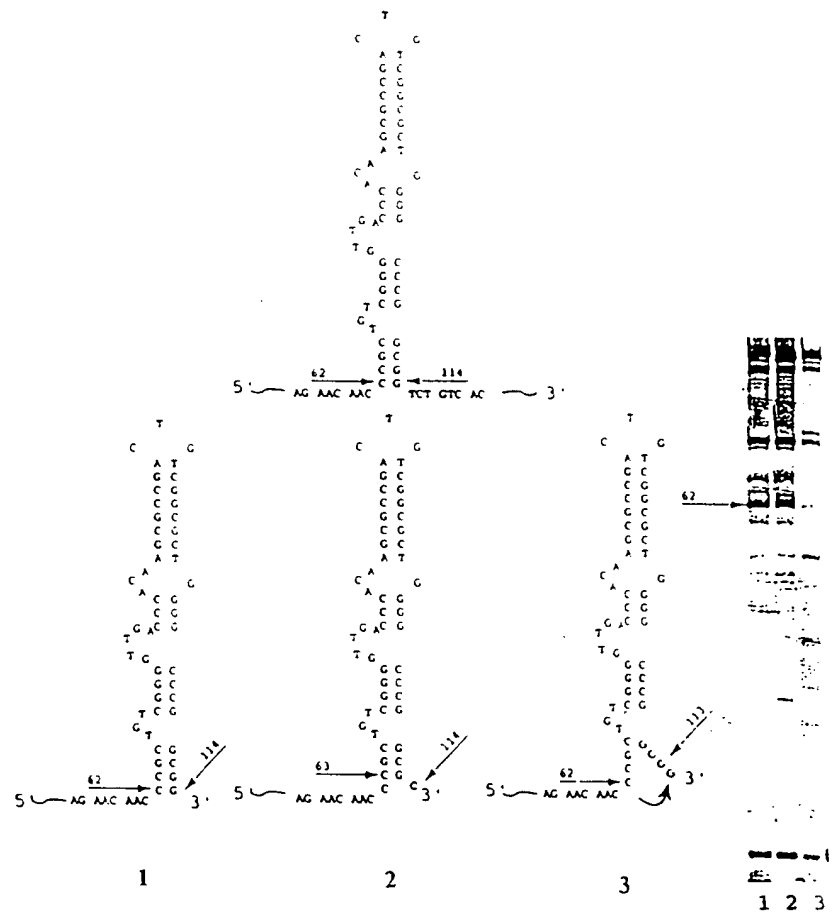
$$\begin{array}{r} 53 \overline{) 123} \end{array}$$


FIGURE 37C

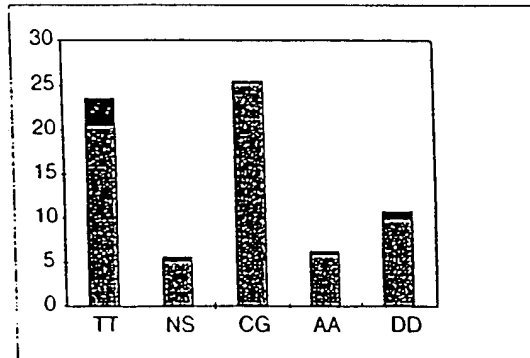
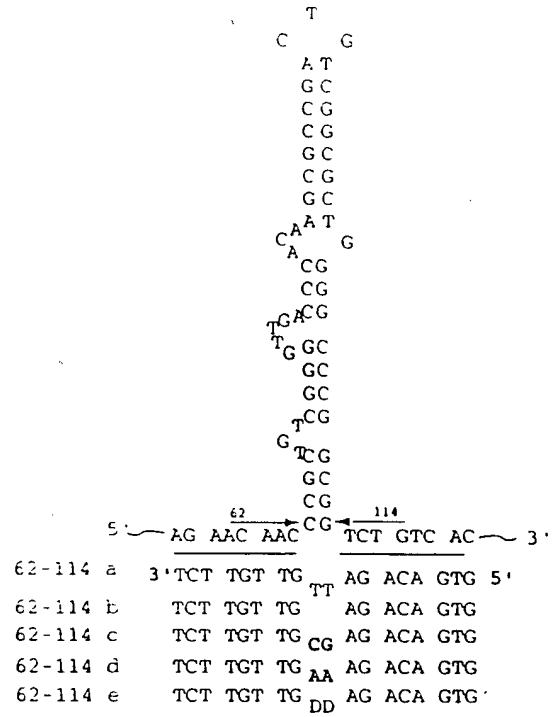


FIGURE 38A

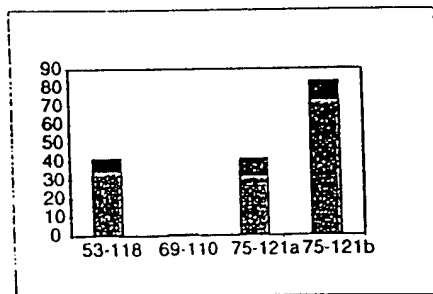
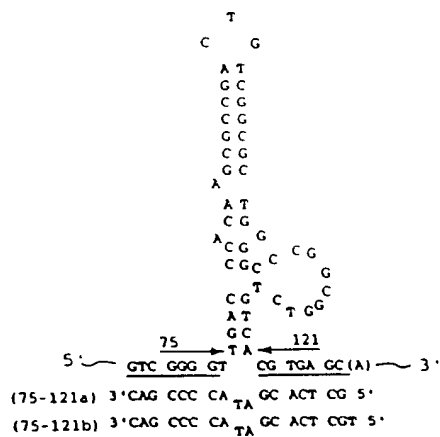
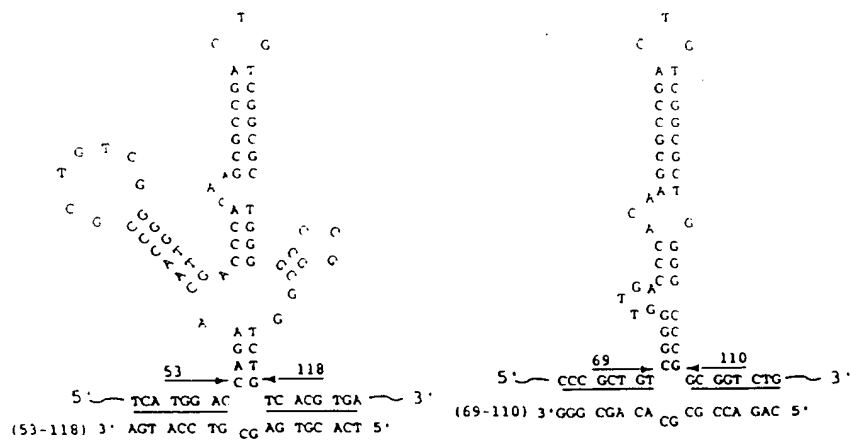


FIGURE 38B

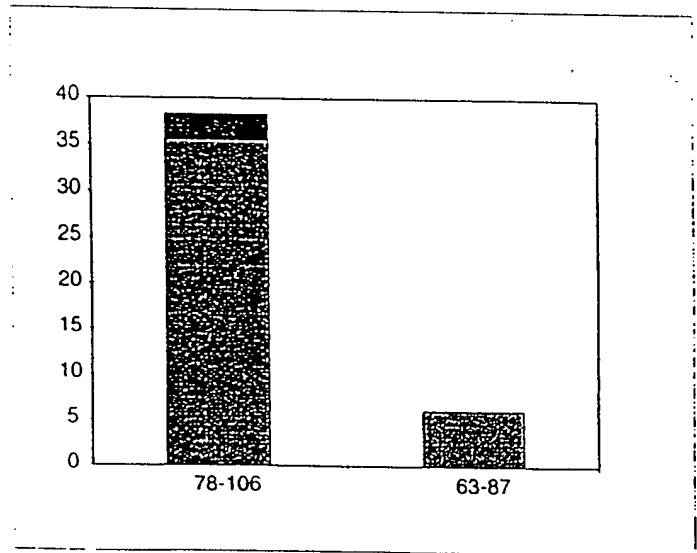
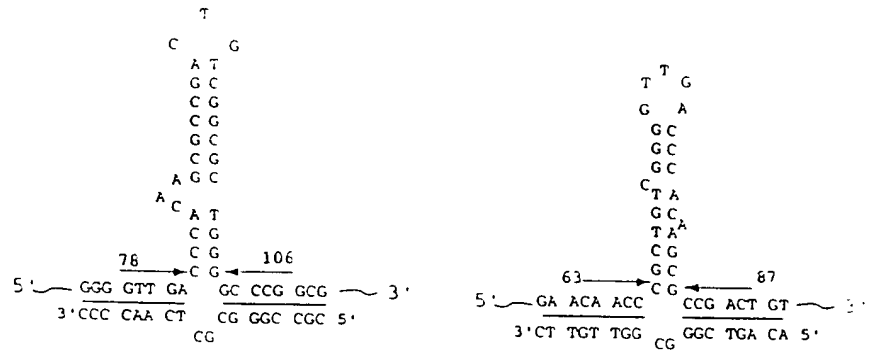
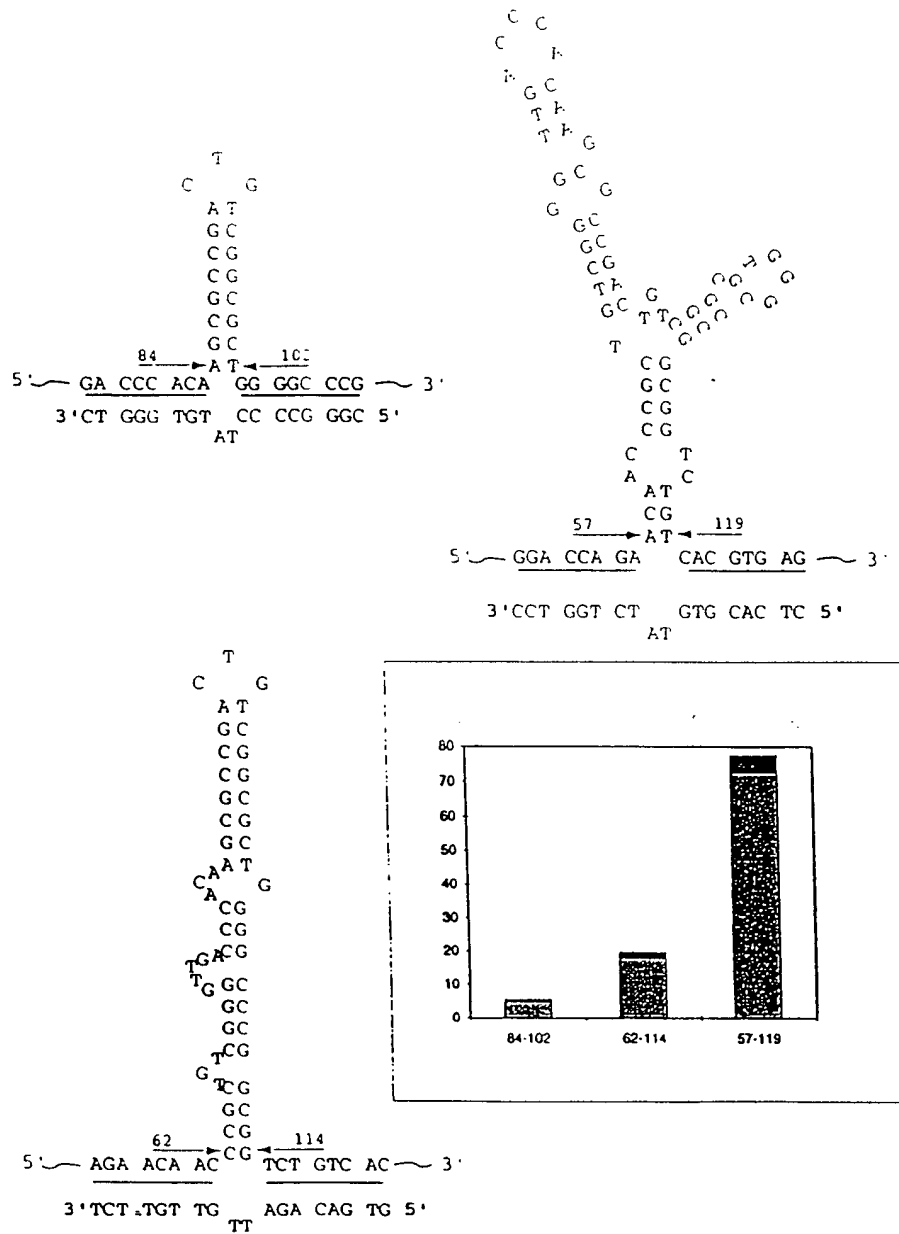


FIGURE 38C



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FIGURE 39

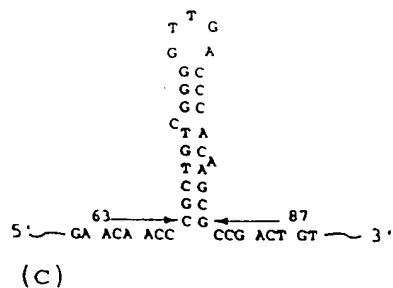
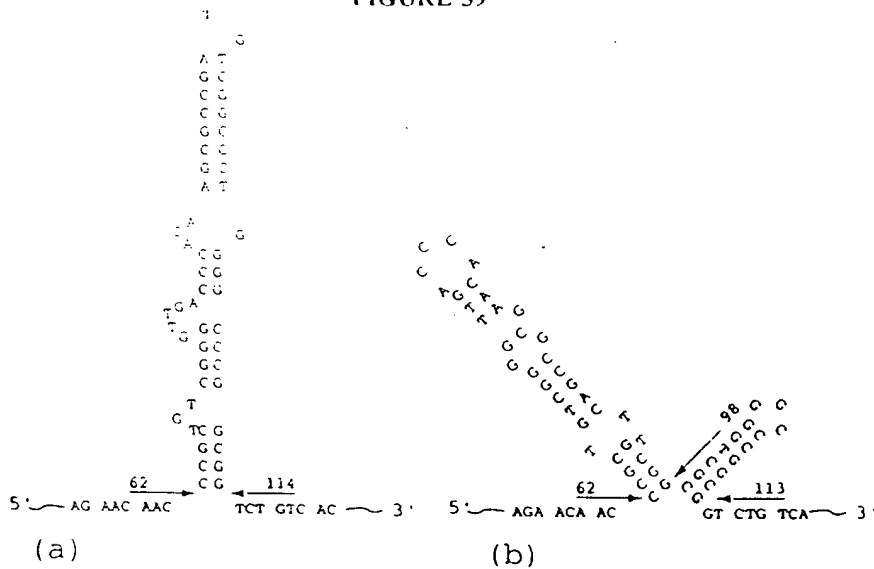
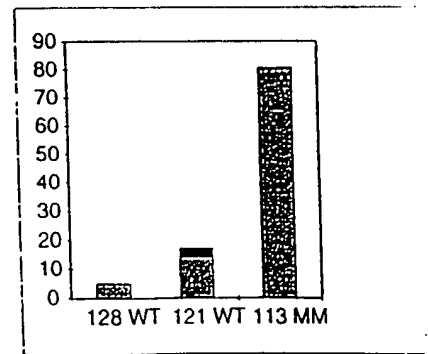
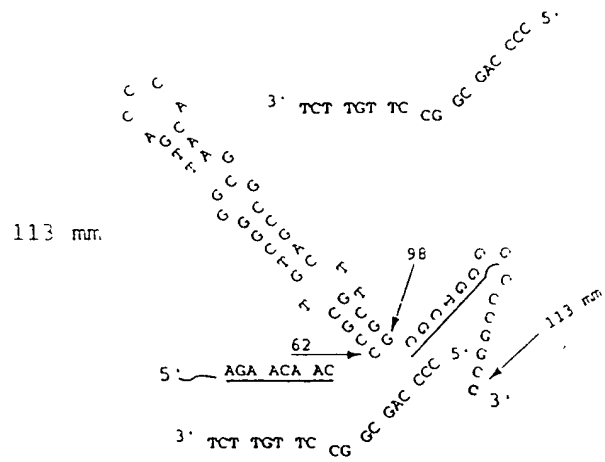
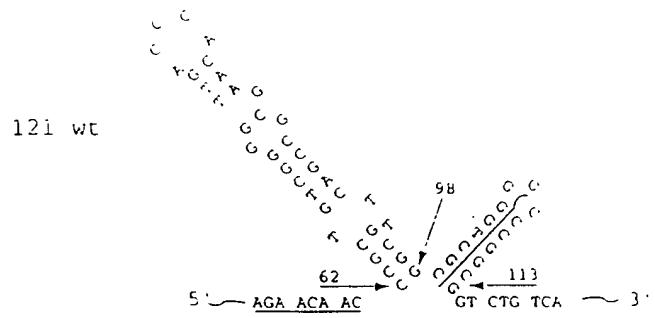


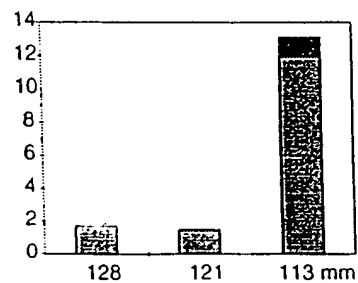
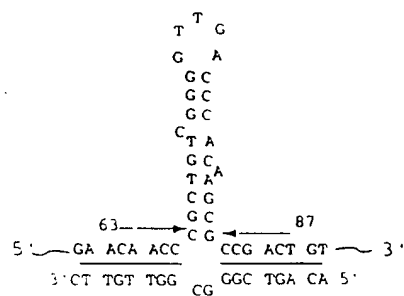
FIGURE 41



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FIGURE 42

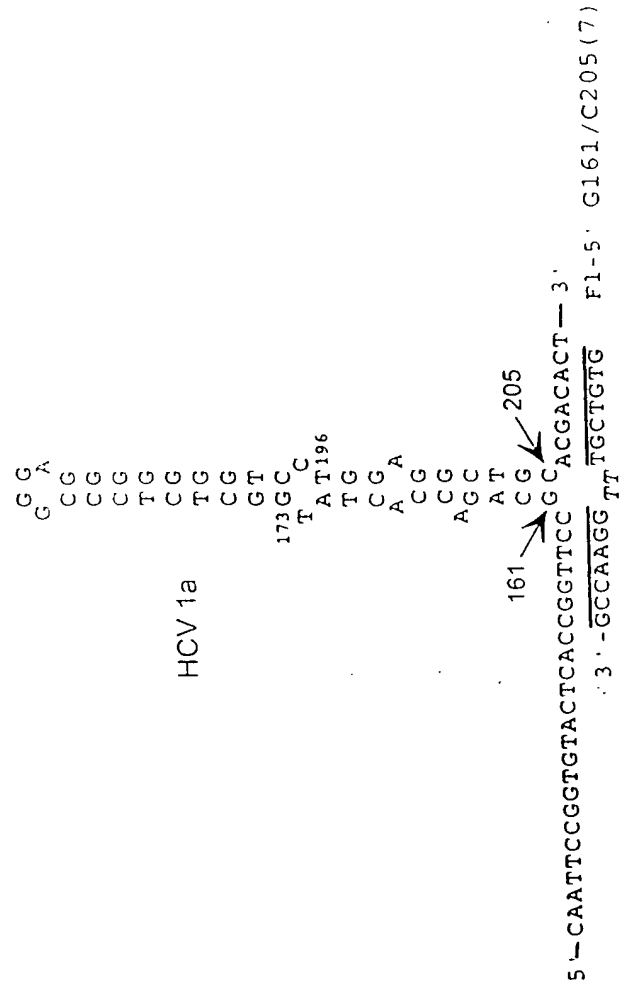
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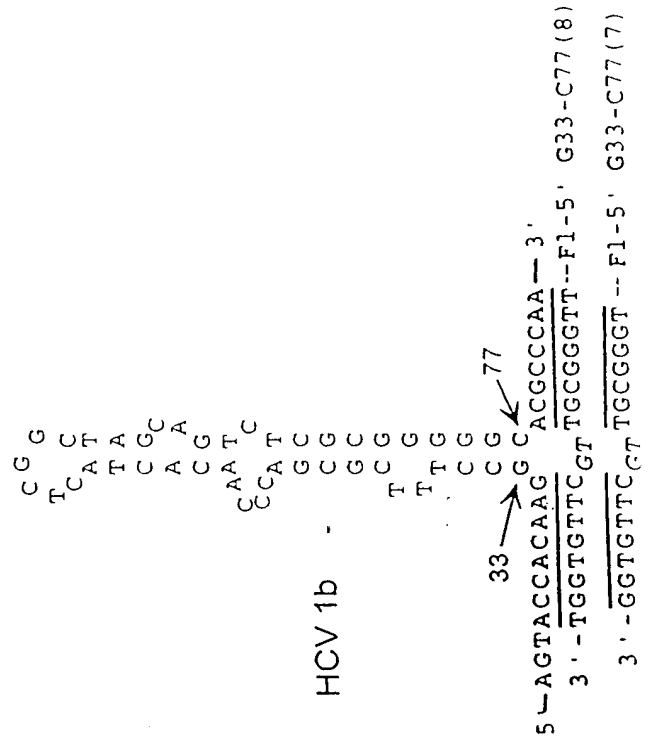
FO5190-5462860

FIGURE 43A



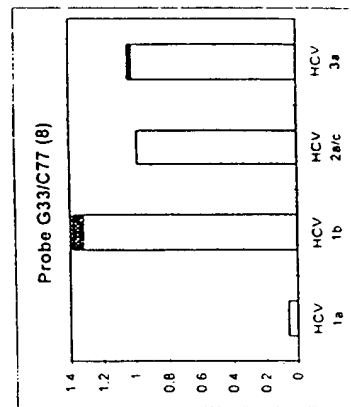
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FIGURE 43B



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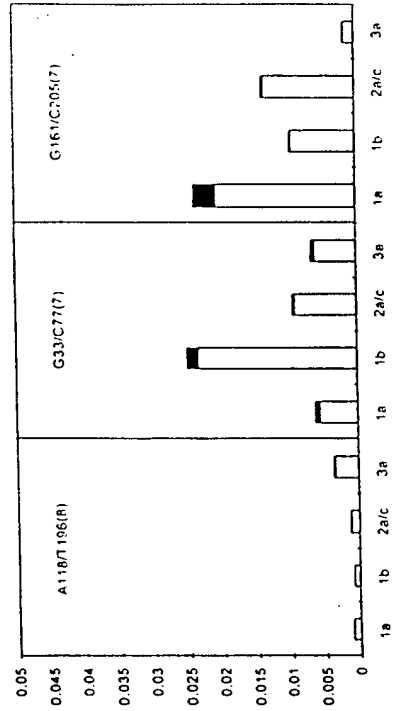
FIGURE 44A



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FIGURE 44B



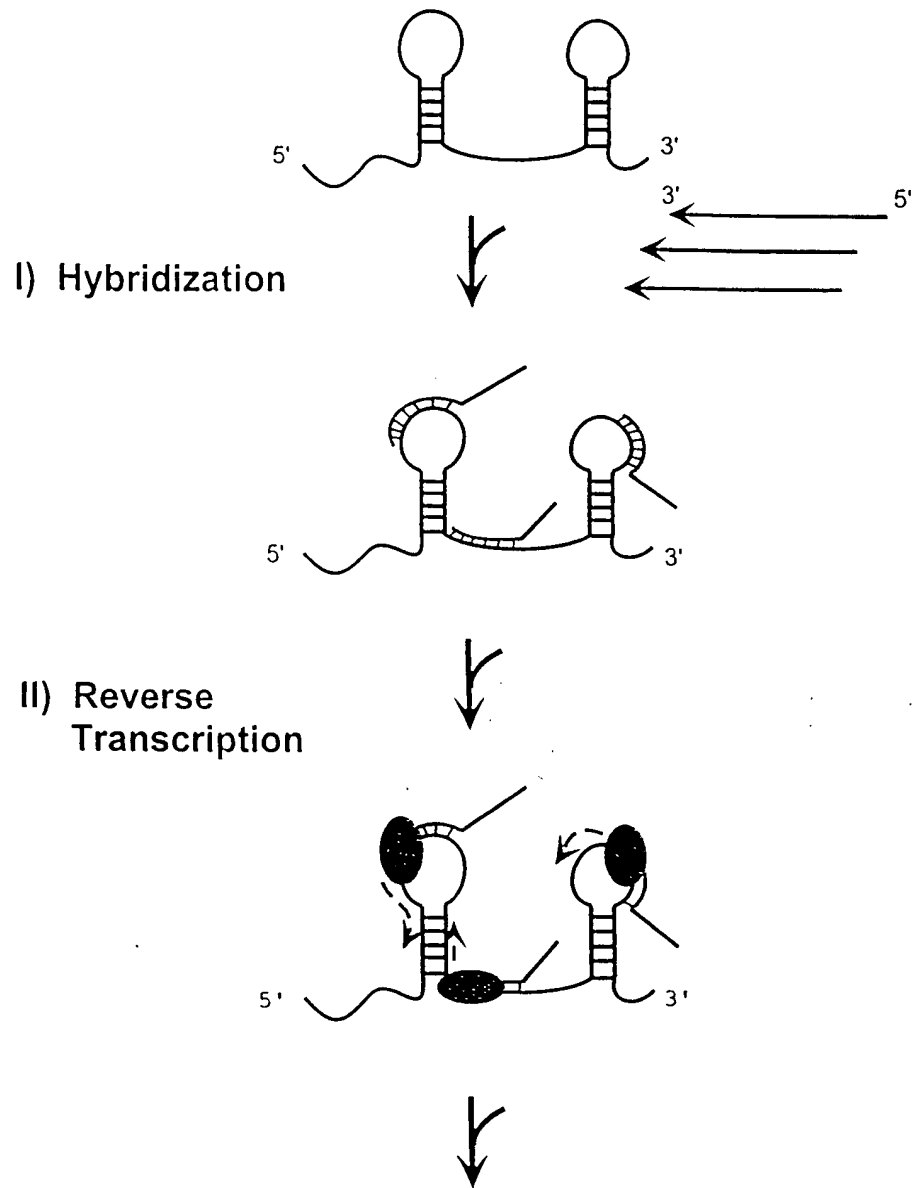
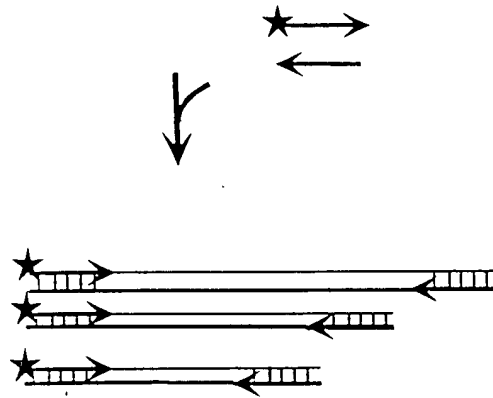


FIGURE 45A

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III) PCR



IV) PAGE with Sequencing Ladder

A C G T RT-Products

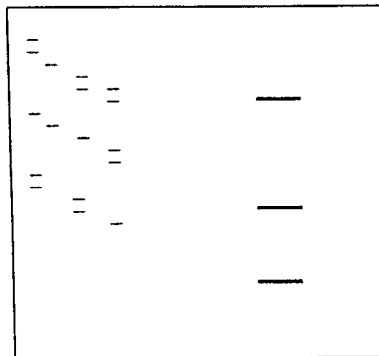
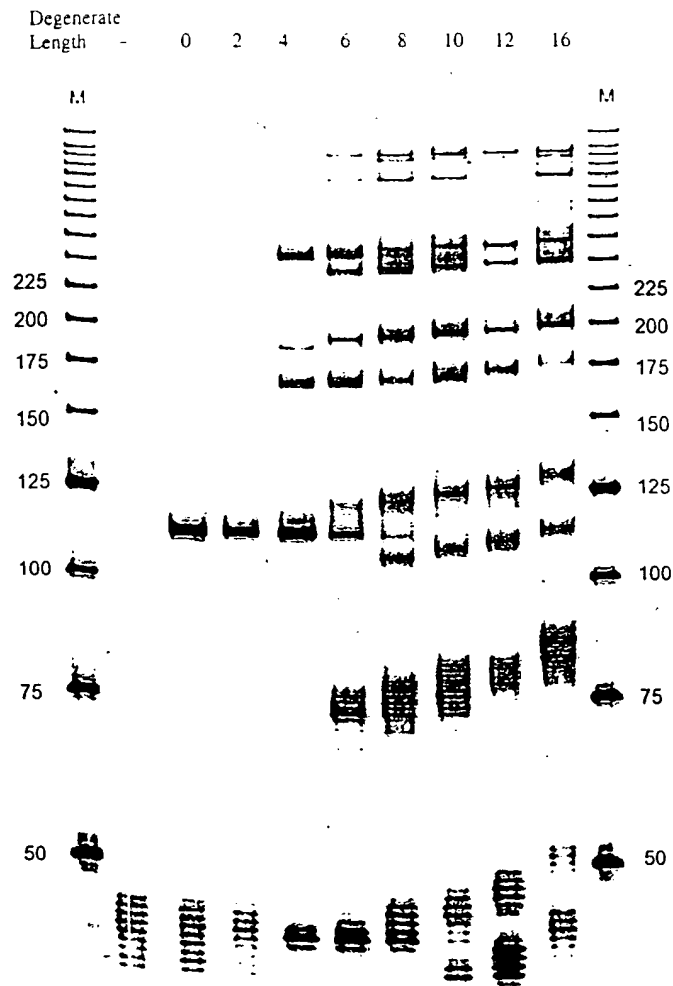


FIGURE 45B

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FIGURE 46



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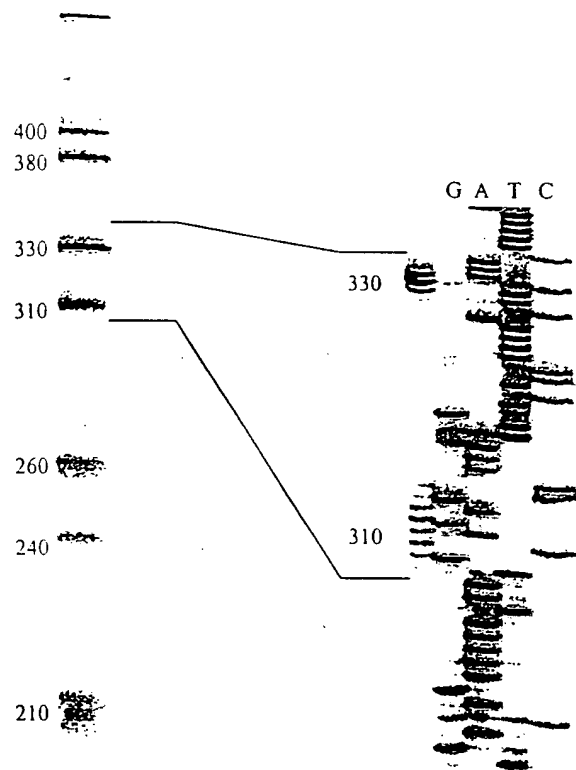


FIGURE 47

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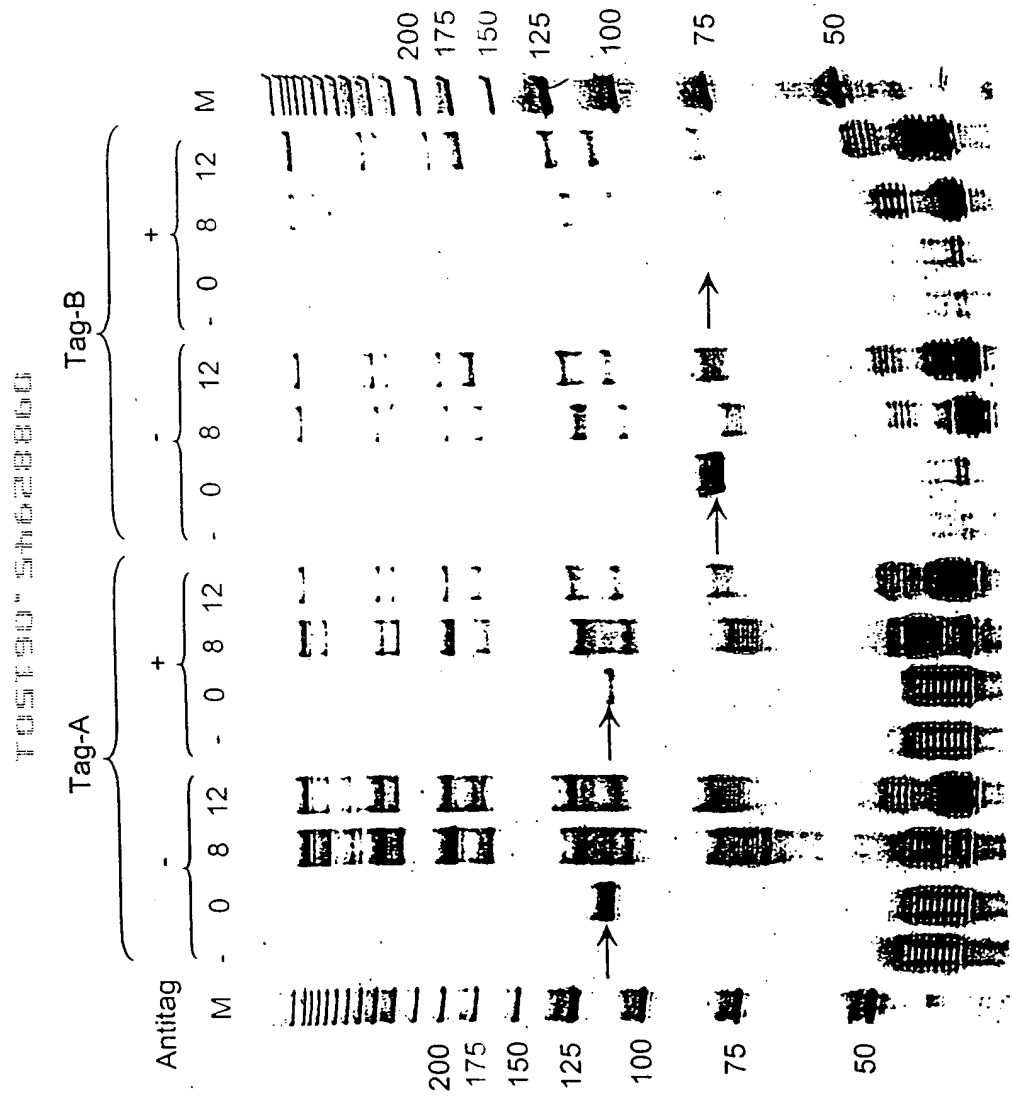


FIGURE 48

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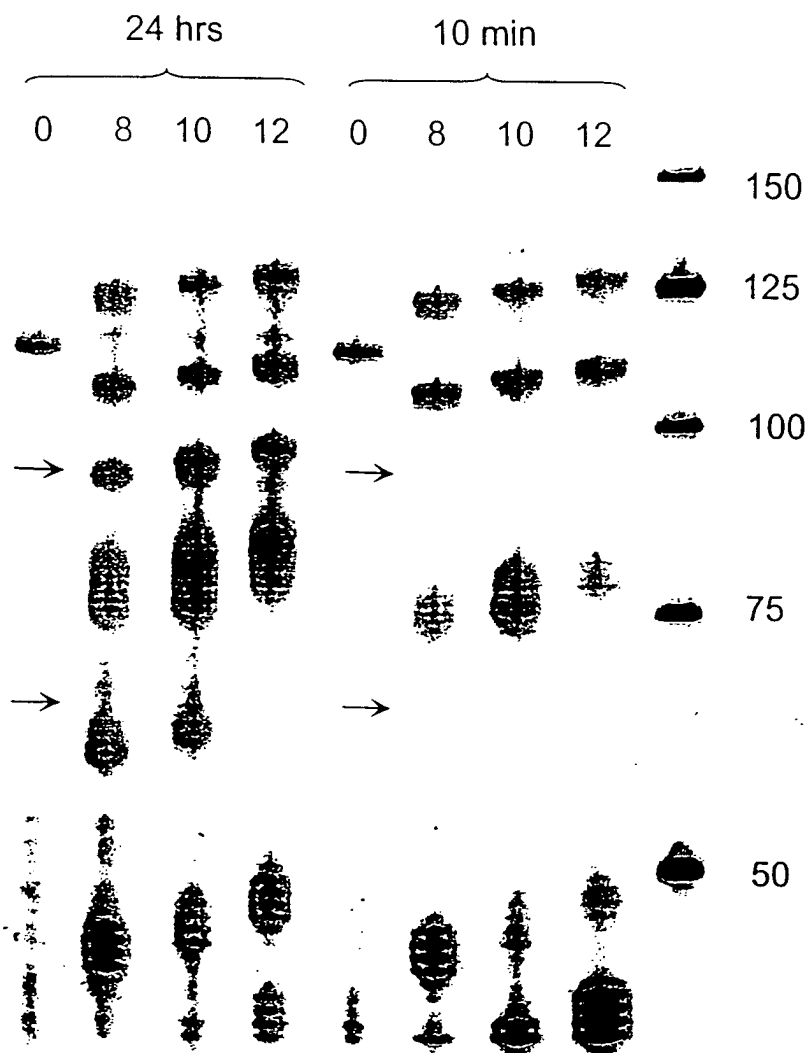


FIGURE 49

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25
 |
 G G G C A
 G C A
 G A
 G A
 G U
 C U
 15 — C — G — 35
 G-C
 C-G
 G-C
 G U
 10 — G G — 40
 U-A
 G-C
 G-C
 U-A
 5 — G U — 45
 G-C
 U C
 G
 G

SEQ ID 142

FIGURE 50A

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105191-51628860

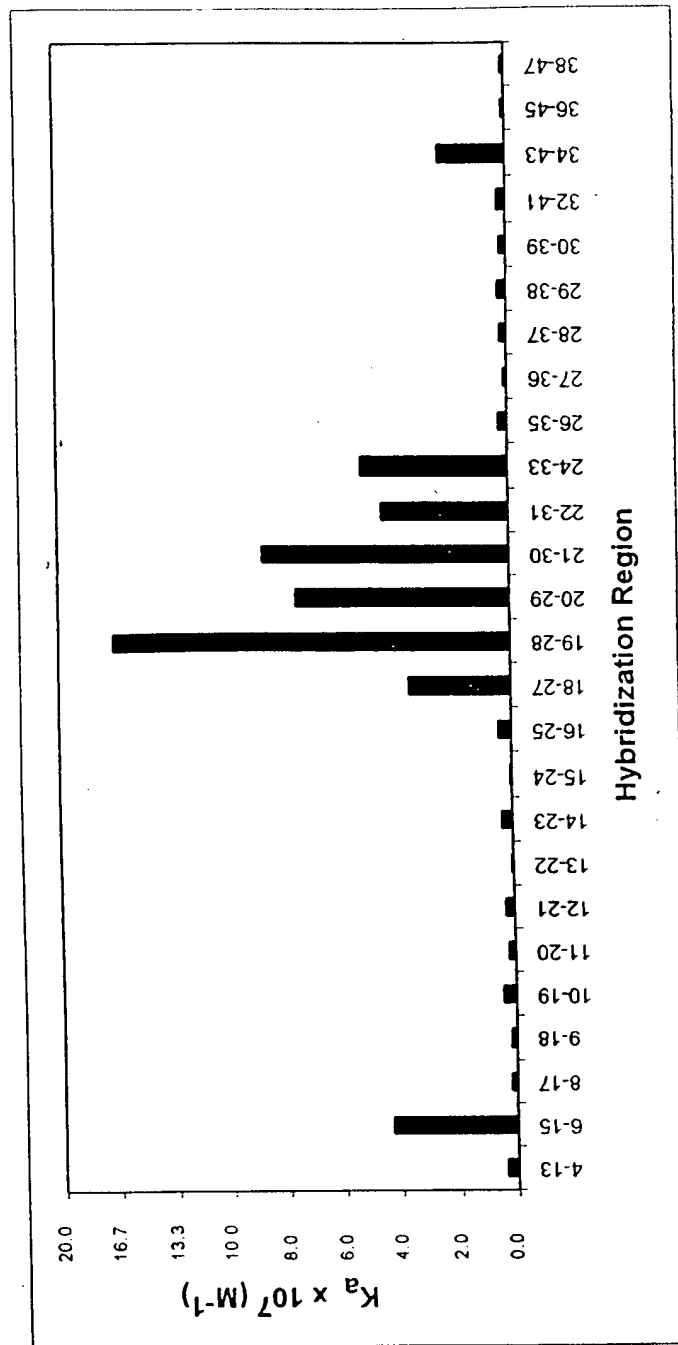


FIGURE 50B

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/123

FIGURE 51

1 ACACUUGCUU UUGACACAAC UGUGUUUACU UGCA**44-50****AAUCCCC** CAAAACAGAC
51 AGAA**64-68****AUGGUGC** AUCUGUCCAG UGAGGAGA**88-97****AAG UCUGCGGUCA** CUGCCCUGUG
101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC
151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

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TOSTER-SHE2860

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FIGURE 52A

ISIS 1571(-) ISIS 3067(+)

1 GCGCCCCAGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT

ISIS 1570(+)

41 GCAACCTCAG CCTCGCTATG GCTCCCAGCA GCCCCCGGCC

81 CGCGCTGCCC GCACTCCTGG TCCTGCTCGG GGCTCTGTTC

121 CCAGGACCTG GCAATGCCCA GACATCTGTG TCCCCCTCAA

161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG

201 CAGCACCTCC TGTGACCAGC CCAAGTTGTT GGGCATAGAG

241 ACCCCGTTGC CTAAAAGGA GTTGCTCCTG CCTGGGAACA

281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934(-)

321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA

361 ACAGCTAAAA CCTTCCTCAC CGTGTA CTGG ACTCCAGAAC

401 GGGTGGA ACT GGCACCCCTC CCCTCTTGGC AGCCAGTGGG

441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGGCA

481 CCCC GGGCCA ACCTCACC GT GGTGCTGCTC CGTGGGGAGA

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521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA

as 610

561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA

601 GCCAATTTCT CGTGCCGCAC TGAAGTGGAC CTGCGGCCCC

641 AAGGGCTGGA GCTGTTTGAG AACACCTCGG CCCCCTACCA

681 GCTCCAGACC TTTGTCTTGC CAGCGACTCC CCCACAACCT

721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG

761 TGGTCTGTTC CCTGGACGGG CTGTTCCCAG TCTCGGAGGC

801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC

841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT

881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT

921 GACGTGTGCA GTAATACTGG GGAACCAGAG CCAGGAGACA

961 CTGCAGACAG TGACCATCTA CAGCTTTCCG GCGCCCAACG

1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

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1041 GACAGTGAAG TGTGAGGCC ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA ACGGGCGCAG

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 ATACACAAGA ACCAGACCCG GGAGCTTCGT GTCCTGTATG

1241 GCCCCCGACT GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGGCCAGAA AATTCCCAGC AGACTCCAAT GTGCCAGGCT

1321 TGGGGGAACC CATTGCCCCG GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTTTCCC ACTGCCCATC GGGGAATCAG TGA CTGTCAC

1401 TCGAGATCTT GAGGGCACCT ACCTCTGTCG GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC ATAATGGGCA CTGCAGGCCT CAGCACGTAC

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```
as 1630    as 1630h(+++)
```

ISIS 1938 (+)

ISIS 1939 (+)

2041 CAGAAGAAGT GGCCCTCCAT AGACATGTGT AGCATCAAAA

Figure 1: Schematic representation of the experimental design. The figure shows a vertical timeline of events. At the top, a horizontal bar represents the 'Time of day' from 0 to 24 hours. Below this, a series of boxes represent different experimental conditions and measurements. The conditions are: 'Control', 'Low dose', 'High dose', and 'Very high dose'. The measurements are: 'Pre-treatment', 'Post-treatment', 'Pre-treatment', 'Post-treatment', 'Pre-treatment', 'Post-treatment', and 'Pre-treatment'. The timeline shows that the 'Control' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements. The 'Low dose' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements. The 'High dose' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements. The 'Very high dose' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements. The timeline also shows that the 'Control' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements. The 'Low dose' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements. The 'High dose' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements. The 'Very high dose' condition is followed by 'Pre-treatment' and 'Post-treatment' measurements.

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ISIS 2302 (+)

2081 CACAAAGGCC CACACTTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA CTGACCCCAA CCCTTGATGA TATGTATTTA

ISIS 1572

2161 TTCATTTGTT ATTTTTACCAG CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT AACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CAAATGGGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTTC TATCGGCACA AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGGTCAGAG ATTACCCAGT

2441 GAGGCCTTAT TCCTCCCTTC CCCCCAAAAC TGACACCTTT

2481 GTTAGCCACC TCCCCACCCA CATACTTTC TGCCAGTGTT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGAATATG CCCAAGCTAT GCCTTGTCTT CTTGTCCTGT

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2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

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105750-5162860

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FIGURE 53A

1 CACAUGUJUC UGAUCAUCUG AAGAUCAGCU AUUAGAAGAG
41 AAAGAUCAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUUAC site 80
81 AAGAACUACU GAUUUCAACU UCUUUGGCUU AAUUCUCUCG site 120
121 GAAACGAUGA AAUAUACAAG UUAUAUCUUG GCUUUUCAGC
161 UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA
201 CCCAUAUGUA CAAGAAGCAG AAAACCUUAA GAAAUUUUU site 210
241 AAUGCAGGUC AUUCAGAUGU AGCGGAUAAU GGAACUCUUU site 240 site 260
281 UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG
321 AAAAAUAAUG CAGAGCCAAA UUGUCUCCUU UUACUUCAAA site 330
361 CUUUUUAAAA ACUUUAAAGA UGACCAGAGC AUCCAAAAGA site 380 site 400
401 GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU
441 CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

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TOST90-SH628260

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481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG

site 560

521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC

site 570

561 AGCAGCUAAA ACAGGGAAGC GAAAAAGGAG UCAGAUGCUG

601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC

641 UACAAUAUUU GAAUUUUAAA UCUAAAUCUA UUUAUUAAUA

681 UUUAACAUA UUUAUAUGGG GAAUAUAUUU UUAGACUCAU

721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG

761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUUA UUUAUUUCC

801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA

site 850

site 860

site 880

841 CUAAUUAGGC AAGGCUAUGU GAUUACAAGG CUUUAUCUCA

site 890

site 910

881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG

921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUAU

961 AAGUGAAGUG AUACUAUCCA GUUACUA

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POST 90-5462860

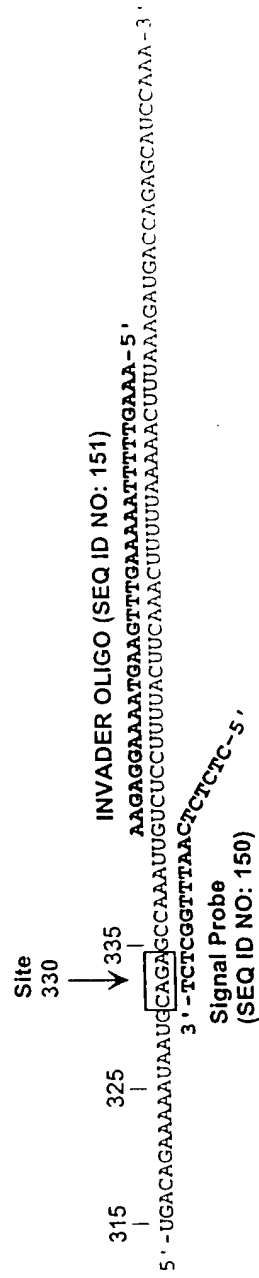


FIGURE 54A

83'
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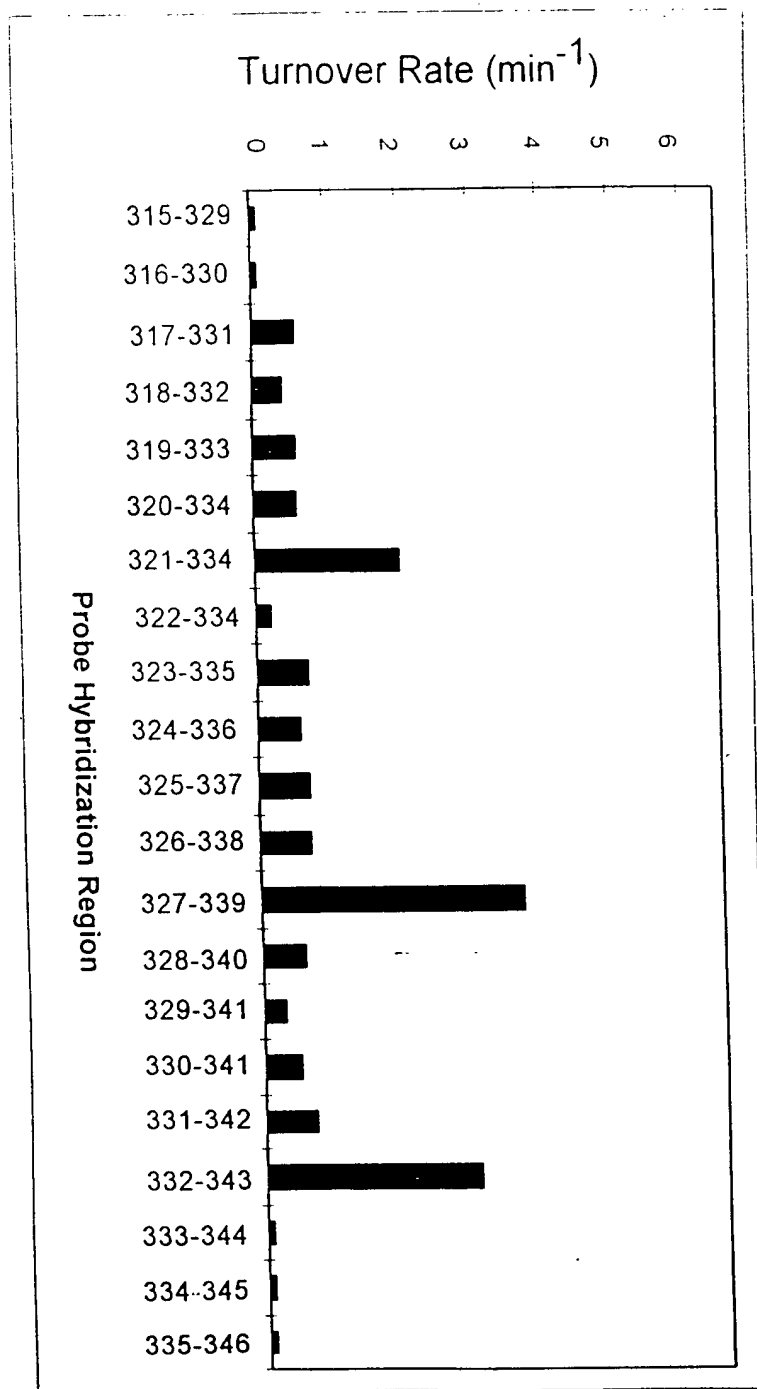


FIGURE 54B
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FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUAA GCGGGGGAGA AUUAGAUCGA UGGGAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUUAAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUAGAA

960 GGCUGUAGAC AAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC

Primer 4

1010 AGAAGACUU AGAUCAUUU AUAAUACAGU AGCAACCCUC UAUUGUGUGC

1060 AUCAAAGGAU AGAGAUAAAA GACAC**CAAGG** AAGCUUUAGA CAAGAUAGAG

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FIGURE 55B

1110 **GAAGAGCAA** **ACALLLGUAL** **GAAAAAAGCA** **CAGCAAGCAG** **CAGCUGACAC**

1160 **AGG**ACACAGC AAUCAGGUCA GCCAAAUAUA CCCUAUAGUG CAGAACAUC

Primer 5

1210 **AGGGGCA**AAU GGUACAUCAG GCCAUAUCAC CUAGAACUUU AAAUGCAUGG

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU

1310 UUCAGCAUUA UCAGAAGGAG CcACCCACACA AGAUUUAAAC ACCAUGC UAA

1360 ACACAGUGGG GGGACAUCAA **GCAGCCAUGC** AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAUGA**GAAG CUGCAGAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGCACCA GGCCAGAUGA GAGAACCAAG GGGAAGUGAC AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCCAGUAG GAGAAUUUA UAAAAGAUGG AUAAUCCUGG GAUUAAAUAA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAU AGACAAGGAC

1660 CAAAGGAACC CUUUGAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCCGAGCAAG** CUUC**ACAGGA** GGUAAAAAAU **UGGAUGACAG** AAACCUUGUU

FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

1810 **CAGCGGCUAC** ACUGAAGAA AUGAUGACAG CAUGUCAGGG AGUAGGAGGA
Primer 8

1860 CCCGGCCAUU AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUAAUGAUGC **AGAGAGGCAA** UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGAAG **GGCACACAGC** CAGAAAUUGC

2010 AGGGCCCCUA GGAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

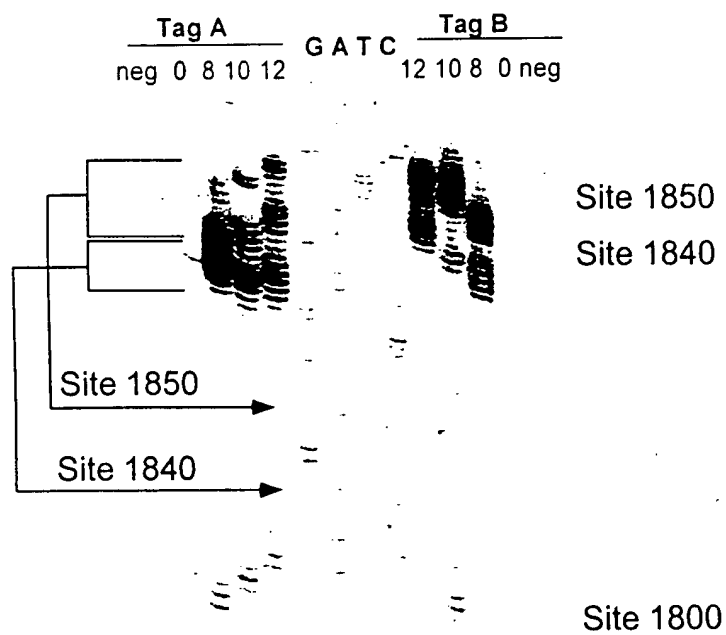
2060 AAUGAAAGAU UGUACUGAGA G

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FIGURE 56

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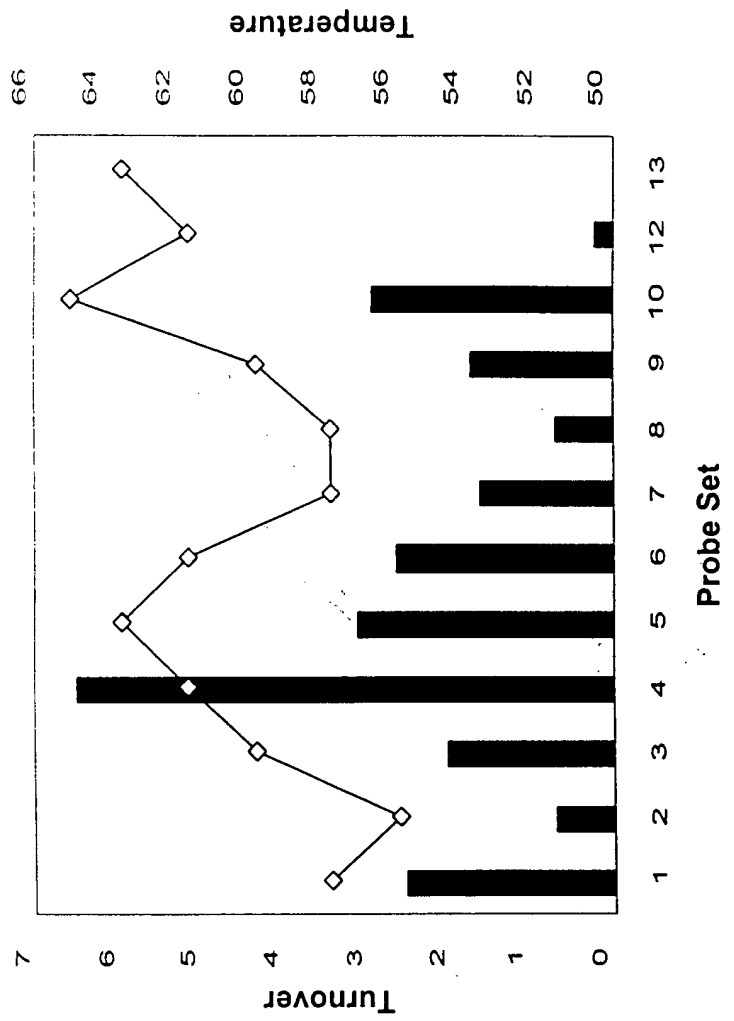
POST 50" 54628860

FIGURE 57

(SEQ ID NO: 188)	CGTATTCCGGTCTCAAAACCGACTTGCT-5'	13
(SEQ ID NO: 187)	AGGTATTCCGGTCTCAAAACCGACT	12
(SEQ ID NO: 186)	ACGGTATTCCGGTCTCAAAACCGAC	10=11
(SEQ ID NO: 185)	CCCGGTATTCCGGTCTCAAAACCGA	9
(SEQ ID NO: 184)	CGCCGGTATTCCGGTCTCAAAACCG	8
(SEQ ID NO: 183)	CGGCCGGTATTCCGGTCTCAAAACC	7
(SEQ ID NO: 182)	AGGCCGGTATTCCGGTCTCAAAAC	6
(SEQ ID NO: 181)	ATGGCCGGTATTCCGGTCTCAAAA	5
(SEQ ID NO: 180)	ACTGGCCGGTATTCCGGTCTCAAA	4
(SEQ ID NO: 179)	ACCTGGCCGGTATTCCGGTCTCAA	3
(SEQ ID NO: 178)	ATCCTGGCCGGTATTCCGGTCTCA	2
(SEQ ID NO: 177)	ACTCCTGGCCGGTATTCCGGTCTC	1
5'-CAUGUCAGGAGUAGGAGACCCGGCCAUAGGCAAGUUUGGCUGAAGCAUGAG-3'		(SEQ ID NO: 158)
1 CAGTCCCTCATC	(SEQ ID NO: 164)	
2 AGTCCCTCATCC	(SEQ ID NO: 165)	
3 GTCCCTCATCCT	(SEQ ID NO: 166)	
4 TCCCTCATCCTC	(SEQ ID NO: 167)	
5 CCTCATCCTCC	(SEQ ID NO: 168)	
6 CCTCATCCTCCT	(SEQ ID NO: 169)	
7 CTCATCCTCCTG	(SEQ ID NO: 170)	
8 TCATCCTCCTGG	(SEQ ID NO: 171)	
9 CATCCTCCTGGG	(SEQ ID NO: 172)	
10 ATCCTCCTGGGC	(SEQ ID NO: 173)	
11 TCCTCCTGGGC	(SEQ ID NO: 174)	
12 CCTCCTGGGCC	(SEQ ID NO: 175)	
13 CTCCTGGGCCGAAA-FL-5'	(SEQ ID NO: 176)	

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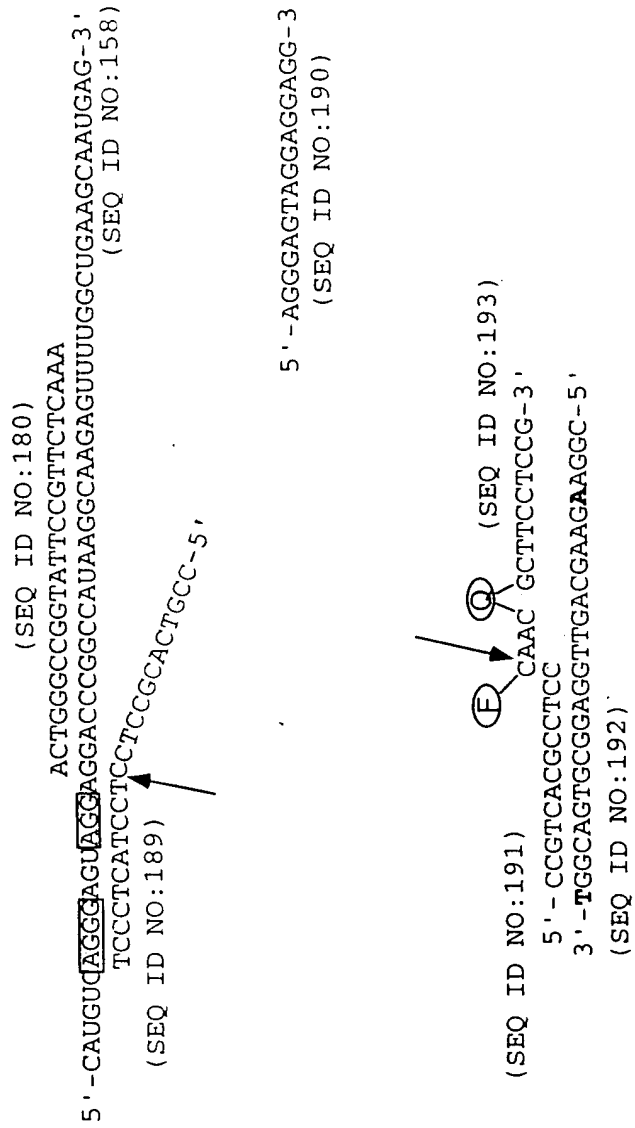
FIGURE 58



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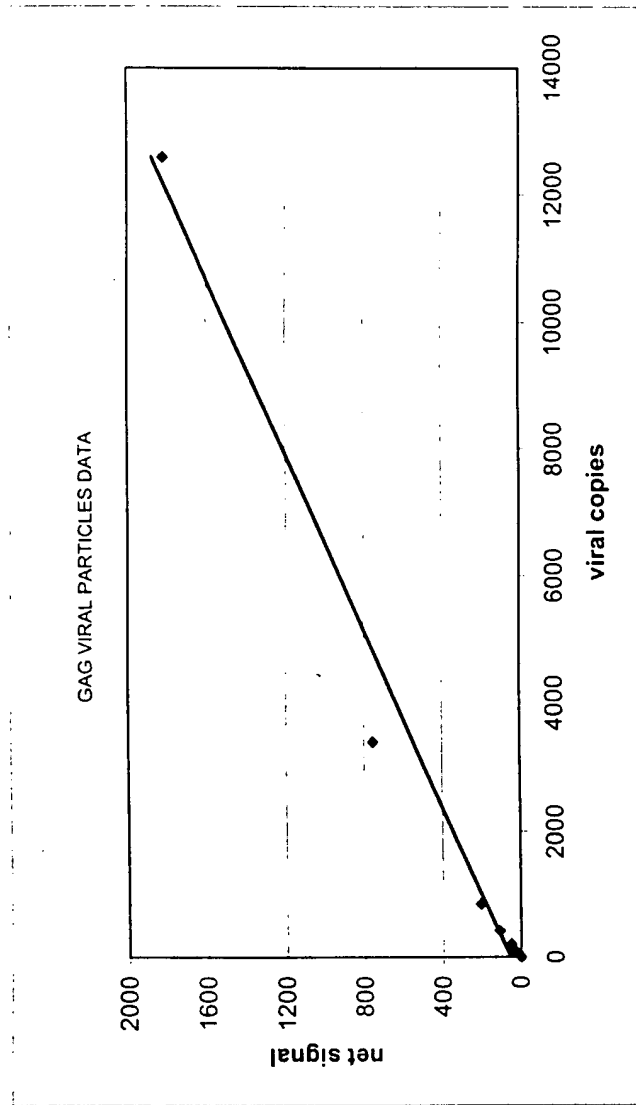
FIG. 59

FIGURE 59



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FIGURE 60



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FIGURE 61A

SEQ ID NO:159

primer 1
3300 AGCUGGACUG UCA AUGACAU ACAGLAGUUA GUGGGGAAAU UGAAUUGGGC
3350 AAGUCAGAUU UACCCAGGGA UUAAGUAAG GCAAUUAUGU AAACUCCUUA
3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUACAGA AGAAGCAGAG
3450 CUAGAACUGG CAGAAAACAG AGAGAUUCUA AAAGAACCAG UACAUGGAGU
primer 2
3500 GUAUU AUGAC CCAUCAAAAG ACUUAUAGC AGAAAUACAG AAGCAGGGGC
3550 AAGGCCAAUG GACAUAUCAA AUUUUAUCAAG AGCCAUUUAA AAAUCUGAAA
3600 ACAGGAAAU AUGCAAGAAU GAGGGGUGCC CACACUAAUG AUGUAAAACA
3650 AUUAACAGAG GCAGUGCAA AAAUAACCAC AGAAAGCAUA GUAAU AUGGG
primer 3
3700 GAAAGACUCC UAAAUUUAAA CUGCCCAUAC AAAAGGAAAC AUGGGAAACA
3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU
3800 UAAUACCCCU CCCUAGUGA AAUUAUGGUA CCAGUUAGAG AAAGAACCCA
3850 UAGUAGGAGC AGAAACCUUC UAUGUAGAUG GGGCAGCUAA CAGGGAGACU
primer 4
3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU AGAGGAAGAC AAAAAGUUGU

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FIGURE 61B

3950 CACCCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC
4000 UAGCUUUGCA GGAUUCGGGA UUAGAAGUAA ACAUAGUAAAC AGACUCACAA
4050 UAUGCAUUAG GAAUCAUUCA **AGCACAACCA** GAUCAAAGUG AAUCAGAGUU
primer 5
4100 AGUCAAUCAA AUAUAGAGC AGUUAUAAA AAAGGAAAAG GUCUAUCUGG
4150 CAUGGGUACC AGCACACAAA GGA**AUUGGAG** GAAUGAACA AGUAGAUAAA
4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGAUAA
4250 GGCCCAAGAU GAACAUGAGA AAUAUCACAG UAAUUGGAGA GCAAUGGCUA
primer 6
4300 GUGAUUUUUA CCUGCCACCU GUAGUAGCAA AAGAAUAGU **AGCCAGCUGU**
4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG
4400 UCCAGGAUAU UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC
4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUAU UAG**AAGCAGA** AGUUAUUCCA
primer 7
4500 GCAGAAACAG GGCAGGAAAC AGCAUAUUUU CUUUUAAAAU **UAGCAGGAAG**
4550 **AUGGCCAGUA** AAAACAAUAC AUACUGACAA **UGGCAGCAAU** UUC**ACCGGUG**
4600 CUACGGUUAG GGCCGCCUGU UGGUGGGCGG GAAUCA**AGCA** GGAAUUUGGA

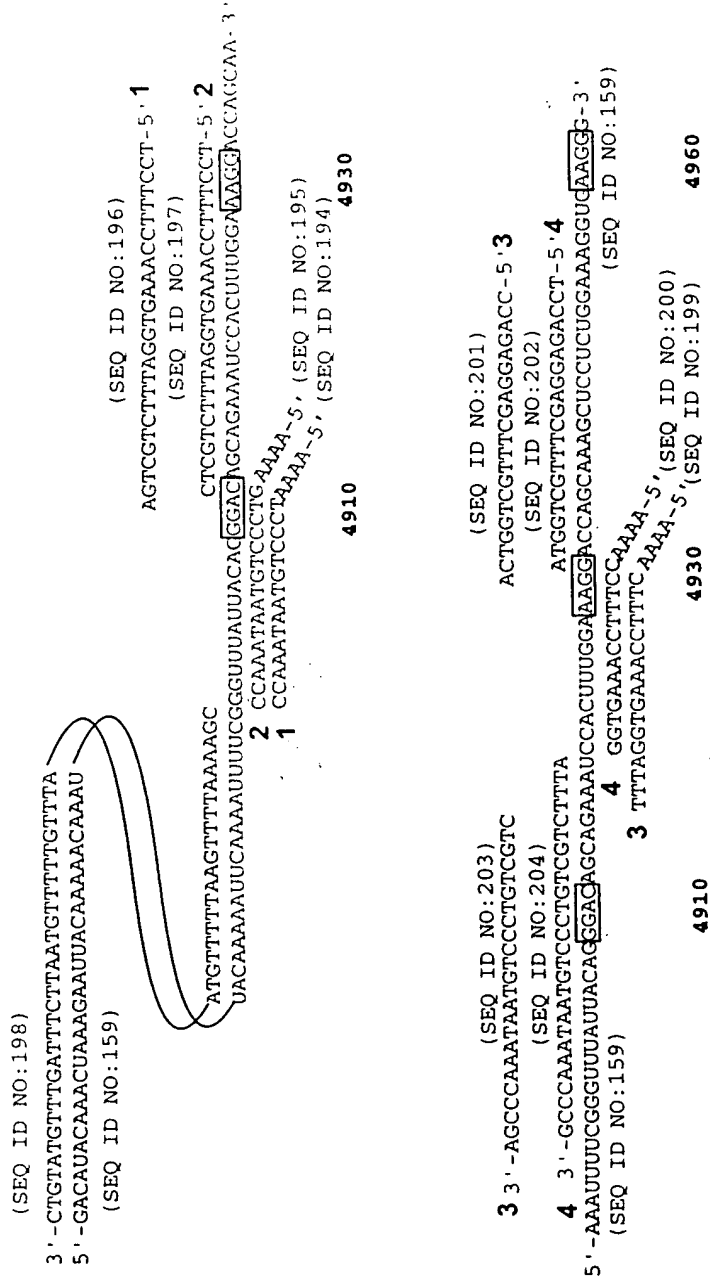
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FIGURE 62



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FIGURE 63

(SEQ ID NO:213)
5 3'-TCCTGGTCGTTTCGAGGAGA (SEQ ID NO:209)
ACCCGTCATCATTTATGTTCTATTATATCACTGTATTTT-5' 5
(SEQ ID NO:214)
6 3'-CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:210)
ACCGTCATCATTTATGTTCTATTATCACTGTATTTT-5' 6
5'-GTAAGGACCCAGCAAGCUCUCUGGAAAGGUAAGGCGAGUAGUAUACAAGAUAGUGACAUAAAUAGUAGU-3'
(SEQ ID NO:159) 5000
4930
5 CTTTCCACTTCCAAA-5', (SEQ ID NO:206)
4960
5 CCTTCCACTTCAAAA-5', (SEQ ID NO:205)

(SEQ ID NO:215)
7 3'-TCGAGGAGACCTTTCCAC (SEQ ID NO:211)
CTCATTATGTTCTATTATCACTGTATTTTCATCACGG-5' 7
(SEQ ID NO:216)
8 3'-TCGAGGAGACCTTTCCACT (SEQ ID NO:212)
ACATTATGTTCTATTATCACTGTATTTTCATCACGG-5' 8
5'-GTAAGGACCCAGCAAGCUCUCUGGAAAGGUAAGGCGAGUAGUAUACAAGAUAGUGACAUAAAUAGUAGU-3'
(SEQ ID NO:159) 5000
4930
7 TTTCCCGTCATAAAA-5', (SEQ ID NO:208)
4960
7 TTTCCCGTCATAAAA-5', (SEQ ID NO:207)

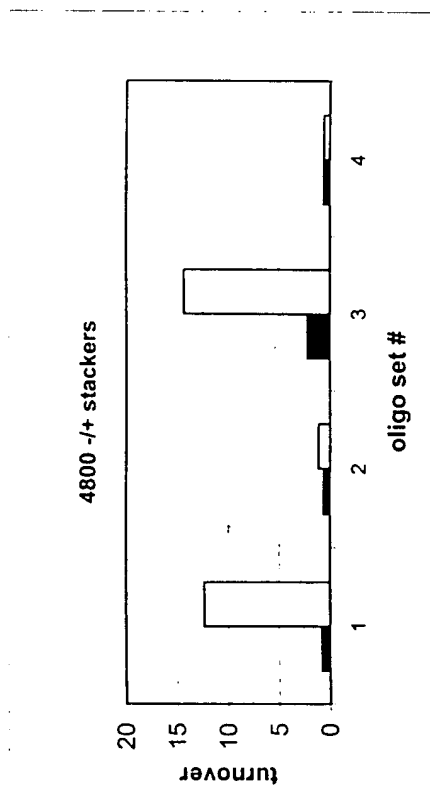
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FIGURE 64

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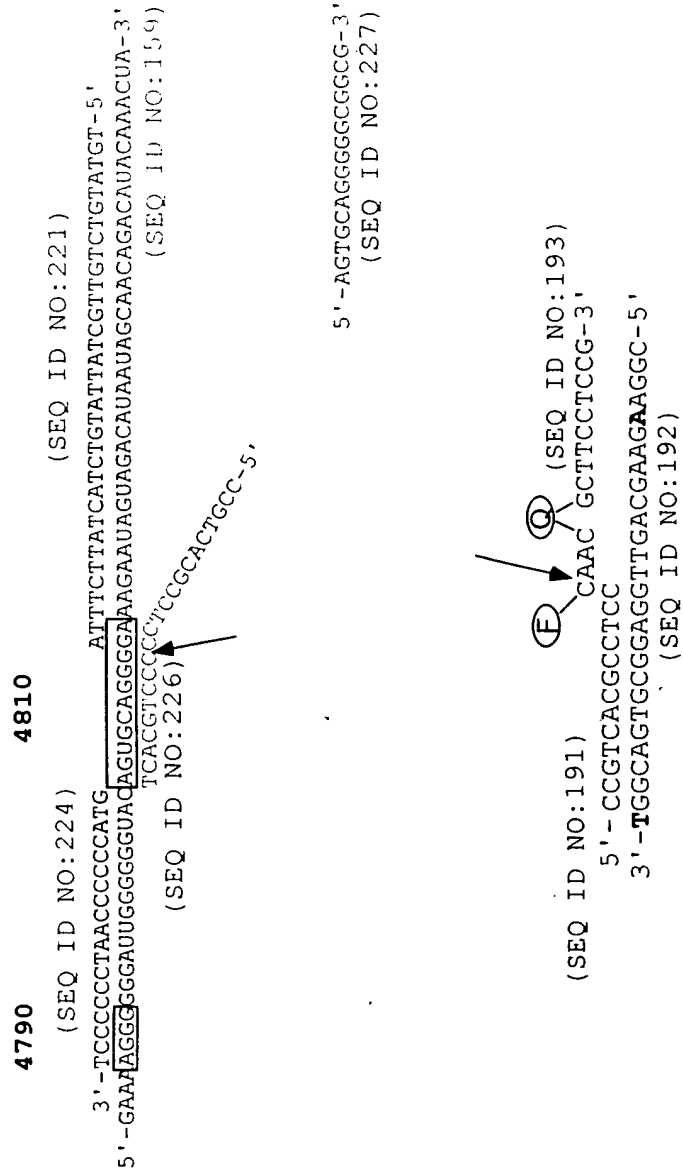
FIGURE 65



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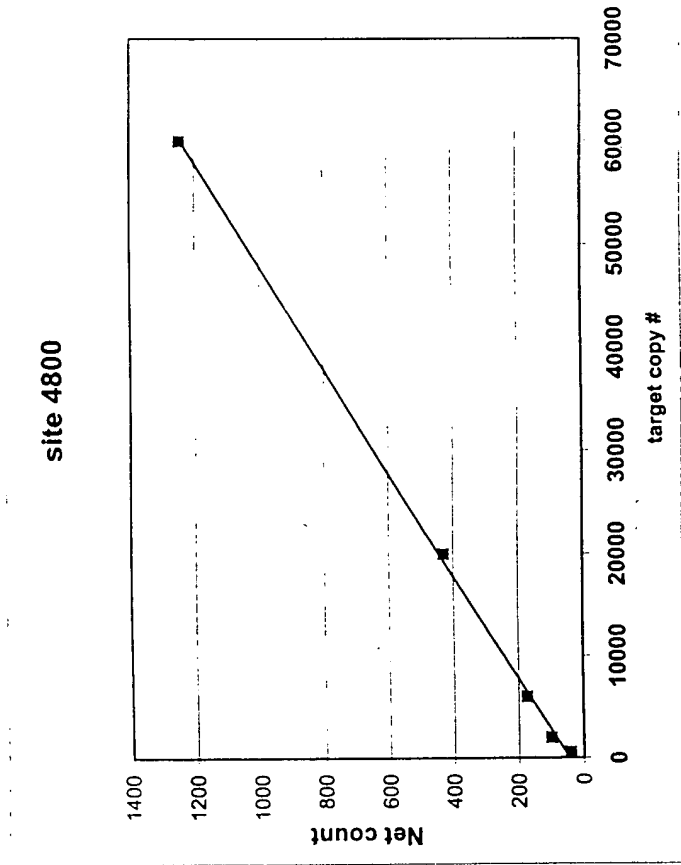
105150" 54628860

FIGURE 66



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FIGURE 67

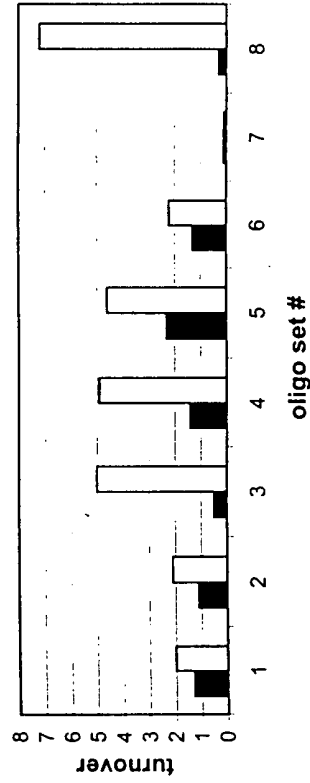


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FIGURE 68

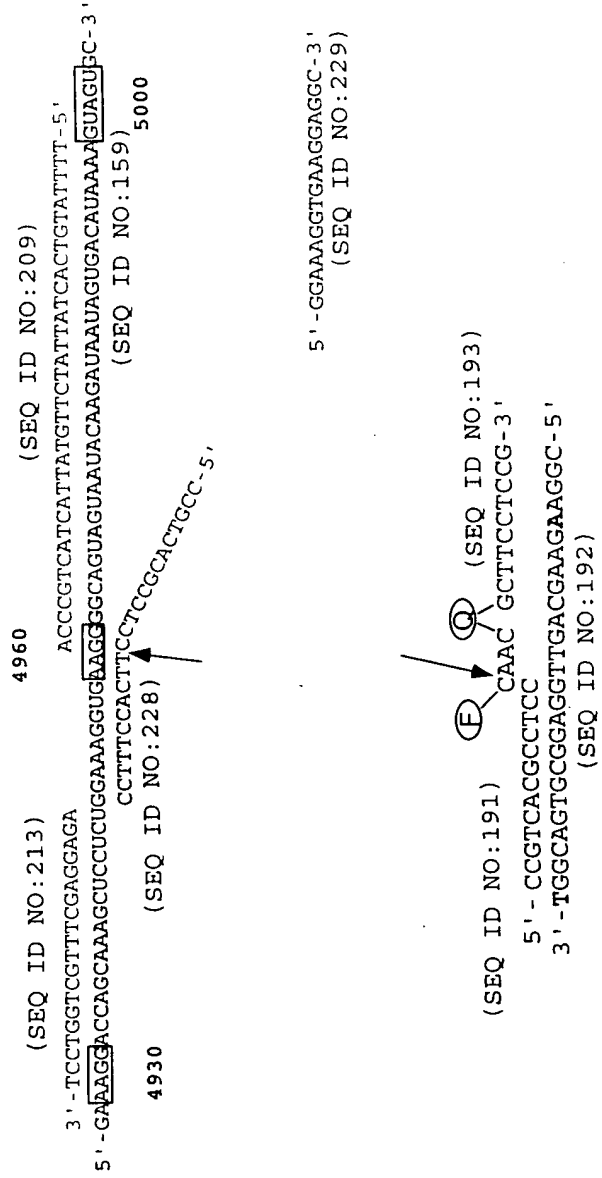
4910-60
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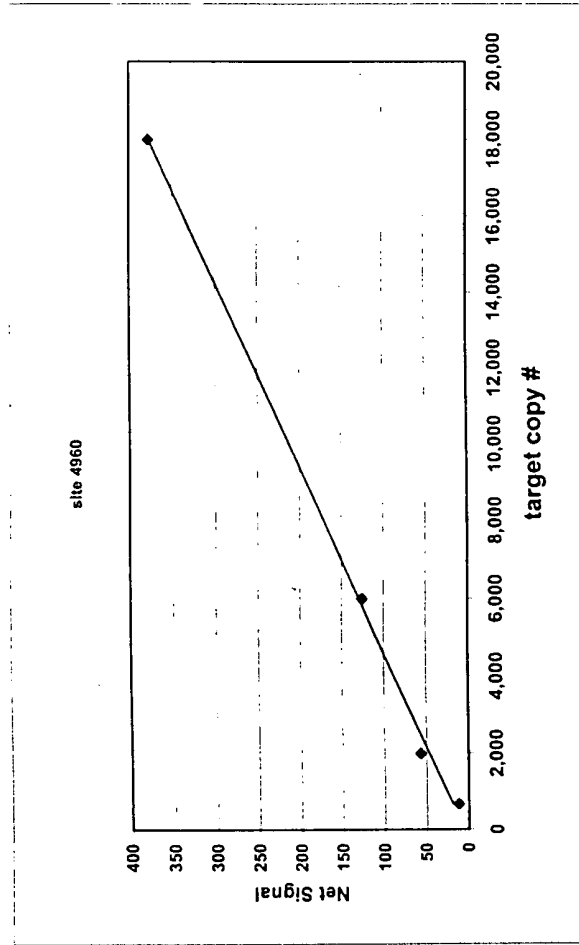
FIGURE 69



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FIGURE 70



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FIGURE 72

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)

520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAUGCAGAUUUUCGUGAAAACCCUUA^{CGG}GGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAAUGUA^{AAAGGC}CAAGAUCAGGAUAAGGAAGGAU
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUAUCUUUGUGUUGAGACUU^{CGUGGUG}G
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAA^{GCU}GGCUGUCCUGAAAUAUUAUAAGGUGGAUAGAGAAUGGC^{AAAAU}UAGUC
GCCUUCGUCGAGAGUGCCCUUCUGAUGAUGUGGUGCUGGGGUGUUUAUGGCAAGUCACU
UUGACAGACAUUAUUGUGGCAAAUGUUGUCUGA

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FIGURE 73

HCV-1a 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCCG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAUAUAGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUAAACCCGCUCAUAGCCUGGAGAUUUGGCGUGCCCGCAAGACUGCUAGCCG
AGUAGUGUUGGUGCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

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FIGURE 74

HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCUCCGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUCAACCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCCCGGAGACUGCUAGCCG
AGUAGUGUUGGUGCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

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FIGURE 76

HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGC
CUAGCCAUGGCGUUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCCUCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUCGUGGGGUGACCGGGUCCUUUC
UUGGAAACACCCGCUCAAUACCCAGAAUUUGGGCGUGCCCCGCGAGAUACUAGCCG
AGUAGUGUUGGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

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FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aaggggaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagtttgcaagaaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtcctgg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagttttggatcctttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caatactgcagatggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccagggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgtttctgcacaga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)

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FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA
GUUUGCAAGAAACAGGUGCUUAACACUAAUUCACCUCCUGAACAAAGAAAUAUGGGCUGU
GACCGGAAUGUGGGCUCAUCGUGGGGUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG
AGGUAUUCUAAUGCCAGUUGGAGACCUGCUUAUCCAAGACAAUAAAAAGCAAGUUG
UCCUCGAAGAAGGUACAAUUGCUUUUAAAAUUGGGUUAAAAAGGCACAGAAGUUUAC
AGACAGUUUUGGAUCUUUGAUGUGCAAAAUCCACAGGAAGUGAUGAUGAACAGCAGCAA
CAUUCAGUUAAGCAAAGAGGUCCUUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA
AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCUGGCAGCCCAAUGGUGCCAUUC
UUUGAACCUCACUACUAGUUGGAAAGAGGCGUGACAACUUCACAGUUCUCAUCUGGC
UGUGGCAGCUGCAUCCCAUAUCUAUCAAUUAUUGUUCAAUGAUCUCAAUUCAC
UUUUUAACAAGUCAAUUCUUAUGUCCAGUCAGAACUUUGAGAGAACUGUUUUGG
GGCUAUAGGGAUCCAUUUUUGAGUUUGGUCCGUACCCUGUUACUACAGUUGGUCUG
UUUUUACCUUACAACAUAUCUGCAGAUUGAGUUUAUAAAGUUUUCAAUGGAAAGAUAA
CAUAAGUAAAGUUGCCAUUAUCGACACAUUAUAAAGGUAUAAAGGAAUCUGUCCUAUUGGG
AAAGUCACUGCGACAUGAUUAUUGGUACAGAUCCAGCCUCAUUUCCACCUUUUGUUGAG
AAAAGCCAGGUUUUGCAGUUCUUUUCUGAUUUUGCAGGUCAAUCUAUGCUGUAUU
UGAAUCCGACGUUAAUCUGAAAGGAAUCCUGUGUAUAGAUUCGUUCUCCAUCCAAAGG
CCUUUGCCUCUCCAGUUGAAAAACCCAGACAACUAUUGUUUCUGCACAGAAAAAUUUC
UCAAAAAAUUGUACAUAUUGGUGUGCUAGACAUCAGCAAUUGCAAAGAAGGGAGACC
UGUGUACAUUUCACUCCUCAUUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA
UGGAUUAAACCCAAAUGAAGAAGAAUAGGACAUACUUGGAUUAUUAACCUAUAACUG
GAUUCACUUUACAUAUUUGCAAAACGGCUGCAGGUCAACCUAUUGGUCAAGCAUCAGAA
AAAAUUAAGUAUUAAAGAAUCUGAAGAGGAACUAUAUUGGCCUAUUCUUUGGCUUAA
UGAGACUGGGACCAUUGGUGAUGAGAAGGCAA

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FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01 5'-ATGGGGTTTGTAAAGTTG-3' (SEQ ID NO:260)
761-47-02 5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3' (SEQ ID NO:261)
937-05-01 5'-TET- atggggtttgttaaagtt-3' (SEQ ID NO:262)
937-05-02 5'-TET- gaagacgacgagagg-3' (SEQ ID NO:263)
937-05-03 5'-TET- ggatgatagttcgtgtg-3' (SEQ ID NO:264)
937-05-04 5'-TET- gctgcagcatattgta-3' (SEQ ID NO:265)
937-05-05 5'-TET- ctgctatttggatgca-3' (SEQ ID NO:266)
937-05-06 5'-TET- gcagaagtacatcgga-3' (SEQ ID NO:267)
937-05-07 5'-TET- gacatgatggaggaga-3' (SEQ ID NO:268)
937-05-08 5'-TET- agaagaaggatcggg-3' (SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUUGUUAAGUUGUUAAGAAUAAGGCUCACUUUAAGAGAUACCAAGUGAAAUU
UAGAAAGACGACGAGAGGGUAAAACUGAUUAUUAUGCUCGGAAACGCUUGGUGAUACAAG
AUAAAAUAAUACACACACCCAAAUACAGGAUGAUAGUUCGUGUGACAAACAGAGAU
AUCAUUUGUCAGAUUGCUUAUGCCCGUAUAGAGGGGGAUAGAUAGUCUGCGCACGUUA
UGCACACGAACUGCCAAAUAUGGUGUGAAGGUUGGCCUGACAAAUAUGCUGCAGCAU
AUUGUACUGGCCUGCUGGUUGCCCGCAGGCUUCUCAAUAGGUUGGCAUGGACAAGAUC
UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUCAG
CCAGGUGCCUUCACCUGCUAUUUGGAUGCAGGCCUUGCCAGAACUACCACUGGCAAUAA
AGUUUUGGUGCCUGAAGGGAGGUGUGGAUGGAGGCUUGUCUAUCCUCACAGUACCA
AACGAUCCCUUGGUUAUGAUUCUGAAAGCAAGGAUUUAUUGCAGAAGUACAUCGGAAG
CACAUCAUGGCCAGAAUGUUGCAGAUACAUGCGCUACUUUAUGGAAGAAGAUGAAGA
UGC UUACAAGAAACAGUUCUCUCAUAUAAAGAACAGCGUAACUCCAGACAUGAUGG
AGGAGAUGUAUAGAAAGCUCAUGCUGCUAUAAGAGAGAAUCCAGUCUAUGAAAGAAG
CCCAAAGAAAGAUUAAAAAGAGAGGUGGAACCGUCCAAAUUGUCCCUUGCUCAGAA
GAAGGAUCGGUAGCUCAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
AGAGCUAAACCCAGC

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FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA

Oligonucleotides

726-39-01	5'-GCTCAAGAATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTTGC-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtggaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggaccctatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caagggtgtttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctgggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

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FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUCC
CCGUCCC[UUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAAC][GAG]GUCCUC
AACGGCCAGAAGCCAGUAGU[CCGGG]AGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA
AAAGGUCAACAUCACCUUCAUAUGA[CAACGACACG]GUGUCCUUCGUGGAGAA[CCGCAGG]C
UCCA[UUC]CAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACA[UUGUACUGCCUAACA
UCUUGGUCCUGGGGGGCUUGAUUUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG
AUGACCUUGGCGCUGGUCACCAUGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA
GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUUUUCUACAACGUACCUC[CAGACAU
GCUUCCCAUAAAGGGCAAAUUGGCCUGUUUGUUGGAUGAACACUCGAAUUC][UGG]GG
UCUUCACUGUCUUC[ACGG]GCGUCCAGAAUUUC[AGCA]GGAUCCAUCUGGUGGACAAAUGG
AACGGACUCAGCAAGAUCGAUUUAU[UGGCAUUCAGAGCA]GUGUAAACAUGAUCAA[UGG]GAC
U[UCCGG]GCAGAUG[UGGG]ACCCUUCA[UGACACC]CGA[AUCCUC]GCGUGAAUUCUUCAGCC
[CGGA]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAUCAAGGGUGUUUGAAGGCAUU
CCCACGUAUCGCUUC[ACGGCC]CCCGAUACUCUGUUUGCCAACGGGUCGUCUACCCACC
CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU
UGGUGCGCCUCUGUUUCUCCCCACCCCCACUUUUAAC[AACGCCGAC]CCUGUGUUGUCAG
AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUCCUUGUUCUAGACA[UCCA][
CCGGU]CACUGGGAUCCCCAUGAACUGUUCUGUGAAGAU[GCAGC][UGA]GCCUCUACAUCAA
AUCUGUCAAGGGCAUCGGGCAAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG
GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCAGCUUCUACACGCAGCUGGU
GCUGAUGCCCCAGGUUCUACUACGCGCAGUAUGUGCUGCUGGGGCUUGGAGGCCUCCU
GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAAUAGCUUUUUGUUUGGA
GUGGUAGUAAAAAGGGCUCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCUGA
UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA
CUAUAAG[CCCC]CCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCG
CUUCUUGAGGACUCUCUAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAU
CACACCGUCCGCACGCACGGCACAUGGAUGCCACGCAUGUGCAAAAACAACUCAGGGA
CCAG

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761-57-01 5'-taatacgaactcactatagggacggaagtccaagagcatcactg-3'
(SEQ ID NO:286)

781-57-03	5'-gcaggtagctggtccgta-3'	(SEQ ID NO:287)
781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
781-65-02	5'-TET-aatggcttctttggg-3'	(SEQ ID NO:289)
781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
781-65-04	5'-TET-tacttcgcgcatcgtc-3'	(SEQ ID NO:291)
781-65-05	5'-TET-cttcttcctagttgtg-3'	(SEQ ID NO:292)
781-65-06	5'-TET-tgcctggcgt-3'	(SEQ ID NO:293)
781-65-07	5'-TET-gactctactaagaacca-3'	(SEQ ID NO:294)
781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
781-85-02	5'-TET-tgattaccccgagg-3'	(SEQ ID NO:298)
781-85-03	5'-TET-acgctgttttcctg-3'	(SEQ ID NO:299)
781-85-04	5'-TET-tgagacacctgtacaa-3'	(SEQ ID NO:300)
781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
781-85-06	5'-TET-caagcgaggaggag-3'	(SEQ ID NO:302)

[illegible]

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GGAAGUCCFAGAGCAUCACUGACAUCUACCUCCUGAACCUGGGCCUUGAGCGGACCAGCUC
UUUGUGGCCACUUUGCCCUUCUGGACUCACUACCUCUACAGCCAUGAGGCCUCCACAA
CGCCAUGUGCAAGCUCACGACUGCUUUUUCUUAUUGGCUUUUUGGGGGCAUAUUC
UCAUCACGUCAUCAGCAUCGACCGGUACCUCCGCCAUCGUCUGGCCCCAACUCCAUG
AACAACCGGACAGUGCAACACGGCGUCACCAUCAGUCUGGGCGUCUGGGCGGGCCAAU
CUUAGUGGCGUCGCCCCAGUUAUGUUCACAAAGAGAAAGGACAACGAAUGUUUGGGUG
AUUACCCCGAGGUCCUGCAGGAAUCUGGCCCUGUCUCCGCAACUCGGAGGUCAACAU
CUGGGCUUCGUCCUGCCCUUGCUUAUCAUGAGCUUUUGCUACUUCCGCAUCGUCCGGAC
GCUGUUUCCUGCAAGAAACCGGAAGAAGGCCAGAGCCAUUAGGCUCAUCCUCUUGGUGGU
UGUUGUCUUCUCCUCUUCUGGACGCCUUAACAACUCGUGAUUUUCCUGGGAGACUCUA
AAUUCUACAACUUCUCCCUAGUUGGGCAUGAAGAGGGACCUGAGGUGGGCCCUAGU
GUGACGGAGACAGUGGCGUUAGCCACUGCUGCCUCAACCCCUUUAUCUACGUUUUCG
UGGGGAAAAGUUCAGAAGGUACCUGAGACACCUGUAACAACAAGUGCCUGGCCGUCCUGU
GCGGUGCUGCCUGUCCACGCCGGCUUCUCAACAGAGUCCAGAGGAGCAGGCAGGACAGC
AUUCUGAGCAGCUUGACUCACUACAAGCGAGGGAGAGGGAUCUCUCCUGCUCUGAAGG
GUCUCCCCGACCCCGACUCUACUAAGAACCAGAGUCCUGCAUCUGACUCUGUGUAAUG
AAAAACAGAUUCACCCCC
CUCCUCCUGCAUUUUUAGUGCAAGAAAACGGACCAGGUACCUGC

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Human Interleukin-1 beta (IL-1 β) Oligonucleotides

gtaatttaatacgaactcactataggggaaggtgcagttttgccaaaggagtgctaaag-3'

(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaacatcat-3'

(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3'

(SEQ ID NO:306)

781-50-02 5'-TET-gagagtggaccacac-3'

(SEQ ID NO:307)

781-50-03 5'-TET-gaatcagtgaagatgcc-3'

(SEQ ID NO:308)

781-50-04 5'-TET-cattgtaccatgaaatatcc-3'

(SEQ ID NO:309)

781-50-05 5'-TET-gaactttaatttcaggaattg-3'

(SEQ ID⁰ NO:310)

781-50-06 5'-TET-ccctagtctgctagc-3'

(SEQ ID NO:311)

781-50-07 5'-TET-ttcaagtgtacttattaacc-3'

(SEQ ID NO:312)

781-72-01 5'-TET-aagctggccgtg-3'

(SEQ ID NO:313)

781-72-02 5'-TET-tgcagttttgccaag-3'

(SEQ ID NO:314)

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FIGURE 81B

Human Interleukin-1 beta (IL-1 β) (GenBank Accession #
M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGAAUGAUGGCUUAUUAACAGUGGCAAUGAGGAUG
ACUUGUUCUUUGAAGCUGAUGGCCUAAACAGAUGAAGUGCUCCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAUUCUCCGACCACACUAACAGCAAGGG
CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUU
CCUGCCACAGACCUUCCAGGAGAAUGACCUAGACACCUUCUUCUUCAUCUUUGAA
GAAGAACCUAUCUUCUUCGACACAUGGGAUAACGAGGCUUAUGUGCACGAUGCACCUGU
ACGAUCACUGAACUGCACGCUCCGGGACUCACAGCAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCUUCCACCUCAGGGACAGGAUAUGGAGCAACAAGUGGUGUUC
UCCAUGUCCUUUGUACAAGGAGAAGAAAGUAAUGACAAAUACCUGUGGCCUUUGGCCUC
AAGGAAAAGAAUCUGUACUGUCCUGCGUGUUGAAAGAUGAUAGCCACUCUACAGCU
GGAGAGUGUAGAUCCCAAAAUUACCAAGAAGAAGAUAGGAAAAGCGAUUUGUCUCAA
CAAGAUAGAAUCAAUAACAAGCUGGAAUUGAGUCUGCCCAGUCCCCAACUGGUAC
UCAGCACCUUCAAGCAGAAAAAUGGCCGUCUCCUGGGAGGGACCAAAGGCGGCCAG
GAUAUAACUGACUUCACCAUGCAAUUGUGUCUCCUAAAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAAUCCUAGGGCUGGCAGAAAGGGAACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUCUGUUGUCUACACCAAUGCCCAACUGCCUGCCUU
AGGGUAGUGCUAAGAGGAUCUCCUGUCCAUCAGCCAGGACAGUCAGCUCUCCUUUA
GGGCCAAUCCACAGCCUUUUGUUAGCCAGGCCUCUCUCACUCUCCUACUCACUUA
AGCCCGCCUGACAGAAACCACGGCCACAUUUGGUUCUAAAGAAACCCUCUGUCAUUCGU
CCCACAUUCUGAUAGCAACCGCUUCCCUAUUUUUUUUUUUUUUUUUUUUUUUUU
UUCAUUGGUCUAAUUUUUCAAAGGGGGCAAGAAGUAGCAGUGUCUGUAAAAGAGCCUA
GUUUUUAAUAGCUAUGGAAUCAAUUCAAUUUGGACUGGUGUGCUCUCUUUUAAUCAAGU
CCUUUAAUUAAGACUGAAAAUAUAUAGCUAGAUUUUUUAAUUGGAAUUAUUUAA
UGAGCAAAUAUCAUACUGUUA

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FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01 5'-TET-GCATCGTTTGGGTCTCTT (SEQ ID NO:316)
448-59-02 5'-TET-ACTTTAAAGATGACCAGAGC (SEQ ID NO:317)
448-79-01 CACATTGTTCTGATCATCTG (SEQ ID NO:318)
448-79-02 CGGTAAGTGAATGTC (SEQ ID NO:319)
448-79-03 TAGTAAGTGAATGTC (SEQ ID NO:320)
448-79-04 GACATTCAAGTCAGTTACCG (SEQ ID NO:321)
498-20-01 AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG
(SEQ ID NO:322)
498-20-02 AATTTAATACGACTCACTATACGGTAAGTGAATGTC
(SEQ ID NO:323)
498-20-03 5'-TET-CACATTGTTCTGATCATCTG (SEQ ID NO:324)
498-20-04 5'-TET-CGGTAAGTGAATGTC (SEQ ID NO:325)
498-40-01 5'-
AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA
(SEQ ID NO:326)
498-40-02 5'-
AGTAATTTACGACTCACTATAGGGACGGTAAGTGAATGTCCAAC
(SEQ ID NO:327)
498-84-01 5'-TET-CATTCAGATGTAGCG (SEQ ID NO:328)
498-84-02 5'-TET-GACTCATCAATCAAA (SEQ ID NO:329)
498-84-03 5'-TET-GATTACAAGGCTTTA (SEQ ID NO:330)

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FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCAUCUGAAGAUCAGCUAUUAGAAGAGAAAGAUCAGUUAAGUCCUUU
GGACCUGAUCAGCUUGA[UACAA]GAACUACUGAUUUCACUUCUUUGG[CUUAAT]UCUCUC
GGAAACGAUGAAAUAUACAAGUUUAUUCUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC
UCUUGGCUGUUACUGCCAGGACCCAUUGUA[CAAGAAGC]AGAAAACCUAAGAAAUAUU
UUAA[UGCAG]GUCAUUCAGAUG[UAGC]GGAUAAUGGAACUCUUUUCUAGGCAUUUUGAAG
AAUUGGAAAGAGGAGAGUGACAGAAAAUAUUG[CAGA]GCCAAAUUGUCUCCUUUUACUU
CAAACUUUUUAAAAACUUUAAAGA[UAGCCAGA]GCAUC[CAAAAG]AGUGUGGAGACCAUCA
AGGAAGACAUGAAUGUCAAGUUUUUCAAUAGCAACAAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUUAUUCGGUAAUCUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGU[CGCCAG]CAGCUAAA[ACAGGGAAGCGAAAAAG]GAGUCAG
AUGCUGUUUCGAGGUCGAAGAGCAUCCAGUAAUGGUUGUCCUGCCUACAAUAAUUGAAU
UUUAAAUCUAAAUCUAAUUUAUAAUUAACAUAUUUAUUGGGGAUAUAAUUUUUAGAC
UCAUCAAUCAAAUAAGUAUUUAUAAUAGCAACUUUUGUGUAAUGAAAUGAAUAUCUAUU
AAUUAUUGUAUUUAUUUAUAAUCCUAUAUCCUGUGACUGUCUCACUAAUCCUUUGUUUU
CUGACUAAUUAU[GCAA]GGCUAUGUGAUU[ACAAG]GCUUUAUC[UCAGGG]GCCAACUA[GGCA]
[GCCAACCUAAG]CAAGAUCCCAUGGGUUGUGUGUUUAUUUACUUGAUGAUACAAGAAC
ACUUAUAAGUGAAGUGAUACUAUCCAGUUACUA

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FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION #
AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAUAAAUUCAGAUUGC
GACACUGUCAAUUGCGGGGAAGCCCUAAGAUAUUAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAUAGCCUGGGUAUAGUAACAAUGUUGAAUAUGAAUCUUUU
GCGAGAUGAAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGACUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUUCUUGCAGUGC UAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION #
X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUUCAGAAAUGGGCCGCGUGUUUUUGACCUGC
UAGUCGAUCUGGCCAGACGUAUCUGUGGGUGGCCAGCGGCGACUAACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGGUUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAAG
CACGGAAGGUAUGGGCUGGCUCUCUGAGUCGGCUUAAAGGUACGUGCCGUCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

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FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUCUAAGUG
AUAUACCGUUGUUUUUUUAGUGGGUAUUCUUUACGCUUUCGUAGGAGCGAGUCCAC
ACUCUUGGAGCAAUCCGGGGUAGUGCCUAAACGCAUUUCUUCAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCCGGA
GCUCGCUCCCUUGGCUCCCUUAUAUAUUUUAACAUCAGAAACAAGACAUAUAAACAUCUA
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAUAUCUCGGGGGUCUU
CCGAUCCUAAUCCAUGAUGAUUACGAACUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG